

GenCore version 5.1.6  
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OR N 2 - Nucleic search, using sw model  
Run July 15, 2004, 07:08:15 ; Search time 23689 Seconds  
(without alignments)  
11664.141 Million cell updates/sec  
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Path 6375  
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Seq IDENTITY NUC  
Gap 10.0 ; Gapext 1.0  
Seq 3470272 seqs, 21671516995 residues  
Table header of hits satisfying chosen parameters: 6940544  
Min B S I length: 0  
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Listing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Result No.	Score	Query Match %	Length	DB	ID	Descripti
1	3580.2	56.2	5653	6	I95540	I95540 Sequence 1 from patent US 5733543
2	3580.2	56.2	5900	6	AX573107	AX573107 Sequence 1 from patent US 5733543
3	3578.4	56.1	5432	6	BD234590	BD234590 Sequence 1 from patent US 5733543
4	3578.4	56.1	5432	6	AX026821	AX026821 Sequence 1 from patent US 5733543
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8	3578.4	56.1	6109	12	TRU90717	TRU90717 Sequence 1 from patent US 5733543
9	3578.4	56.1	6180	6	AX207724	AX207724 Sequence 1 from patent US 5733543
10	3578.4	56.1	6195	6	BD168975	BD168975 Sequence 1 from patent US 5733543
11	3578.4	56.1	6238	6	BD168966	BD168966 Sequence 1 from patent US 5733543
12	3578.4	56.1	6277	12	AX437644	AX437644 Sequence 1 from patent US 5733543
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16	3578.4	56.1	6338	6	AR428934	AR428934 Sequence 1 from patent US 5733543
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36	3578.4	56.1	6980	6	AX209897	AX209897 Sequence 1 from patent US 5733543
37	3578.4	56.1	7000	6	E36261	E36261 Human genome
38	3578.4	56.1	7000	6	AX001325	AX001325 Sequence 1 from patent US 5733543
39	3578.4	56.1	7053	6	AX207767	AX207767 Sequence 1 from patent US 5733543
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42	3578.4	56.1	7093	6	AX207736	AX207736 Sequence 1 from patent US 5733543
43	3578.4	56.1	7108	6	E36262	E36262 Human genome
44	3578.4	56.1	7108	6	AX001326	AX001326 Sequence 1 from patent US 5733543
45	3578.4	56.1	7148	6	BD268203	BD268203 Sequence 1 from patent US 5733543

ALIGNMENTS

RESULT 1  
LOCUS I95540 5653 bp DNA linear PAT 15 JUL 1998  
DEFINITION Sequence 1 from patent US 5733543.  
ACCESSION I95540  
VERSION I95540.1 GI:3940010  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5653)  
AUTHORS Nabel, G.J., Woffendin, C., Yang, N.-S. and Sheehy, M.J.  
TITLE Introduction of HIV-protective genes into cells by particle-mediated gene transfer  
JOURNAL Patent: US 5733543-A 1 31-MAR-1998;

## Location/Qualifiers

1. .5653  
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/mol\_type="unassigned DNA"

56.2%; Score 3580.2; DB 6; Length 5653;  
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Conservative 0; Mismatches 63; Indels 470; Gaps 7;

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QY 2649 ----GATCAAGAGACAGGATGAGATCGTTTCGCATGATGAAACAGATGGAT  
DB 2328 ATCTGATCAAGAGACAGGATGAGATCGTTTCGCATGATGAAACAGATGGAT  
QY 2705 AGGTTCTCCGCGCGCTTGGGTGAGAGGCTATTCGGCTATGACTGGGCAACAC  
DB 2388 AGGTTCTCCGCGCGCTTGGGTGAGAGGCTATTCGGCTATGACTGGGCAACAC  
QY 2765 CGGCTGCTCTGATGCGCGCTGTTCCGGCTGTCAAGCGAGGCGCGCGGTTTC  
DB 2448 CGGCTGCTCTGATGCGCGCTGTTCCGGCTGTCAAGCGAGGCGCGCGGTTTC  
QY 2825 CAAAGCGACCTGTCCGCTGCCCTGAAATGAACTGCAAGAGAGGCGAGCGGCT  
DB 2508 CAAAGCGACCTGTCCGCTGCCCTGAAATGAACTGCAAGAGAGGCGAGCGGCT  
QY 2885 GCTGGCCACGACCGGCGCTTCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAG  
DB 2568 GCTGGCCACGACCGGCGCTTCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAG  
QY 2945 GGACTGGCTGTCTATTTGGGCGAAGTCCCGGGCAGGATCTCTGTCTCATCTCACT  
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QY 3065 TACCTGCCCATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGCTACTCC  
DB 2748 TACCTGCCCATTCGACCAACCAAGCGAAACATCGCATCGAGCGAGCAGCTACTCC  
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QY 3185 ACTGTTCCGCGAGCTCAAGGCGAGCATGCCGACAGCGAGGATCTCTGCTGTGAC  
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DB 3209 -----  
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DB 3209 -----  
QY 3665 ACAGGAGAGACATACCGGAGGAAACCGCGCATGACGGCAATAAAGAC  
DB 3209 -----

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DE	1207	-	-	-	-	3208
QY	1847	C	CCCCACCCCCAAAGTTCGGGTGAAGGCCACAGGCTCGCAGCCAACTCGCGGGCGGCAG	3904		
DE	1209	-	-	-	-	3208
QY	1903	G	CCCTGCCATAGCCTCAGTGTACGAGATTTTCGATTTCAGATTCAGCGCGCCCTTCTATGAAGGT	3964		
DE	1209	-	-	-	-	3246
QY	1963	T	GGCTTCGGAATCGTTTTCCGGGACCGCGCTGGATGATCCTCAGCGCGGGGATCTCA	4034		
DE	1209	-	-	-	-	3306
QY	1021	T	CTGAGATTTCTTGGCCACCCCAACTTGTTTATTTGCAGCTTATTAATGTTTACAAATAAA	4084		
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DE	1336	G	CAATAGCATCAAAATTTCAAAAATAAGCATTTTTTTTCACTGCATTTCTAGTTGTGTT	3426		
QY	4147	T	GTCCAAACTCATCAATGATATCTATCATGTCTGTATACCGTCGACCTCTAGCTAGAGCT	4204		
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DE	1360	T	CACATTAATTTGGTTCGGCTCACTGCCCCCTTTCAGTTCGGAAACCTGTCTGCCAGC	3662		
QY	4387	T	GCAATTAATGAATCGGCCAACCGCGCGGGGAGAGCGGTTTTCGTTATTTGGCGCTCTTCG	4444		
DE	1366	T	GCAATTAATGAATCGGCCAACCGCGCGGGGAGAGCGGTTTTCGTTATTTGGCGCTCTTCG	3722		
QY	4447	T	CTCTCGCTCATCTGACTCGCTCGGCTCGGTTCGCTTCGGCTTCGGCGGCGGATCAGCTC	4504		
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Qy	5825	TTGTCCAGAAAGTAAAGTTGGCCG	CAGTGTATCACTCATGGTTATGGCAG	CACTG	5884
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3107 5900 bp DNA linear PAT 29-NOV-2002
ence 2 from Patent WO02059338.
3107
3107.1 GI:26005046
helic construct
helic construct
ficial sequences.

erford, C., Gray, J. T., Lee, J. S. and Mulligan, R. C.
oviral vectors for transduction into quiescent cells and
aging systems for them
nt: WO 02059338-A 2 01-AUG-2002;
Children's Medical Center Corporation (US) ; PRESIDENT AND
OWS OF HARVARD COLLEGE (US)
Location/Qualifiers
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56.2%; Score 3580.2; DB 6; Length 5900;
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Conservative 0; Mismatches 63; Indels 470; Gaps 7;

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1795 CGCGGCTTTCCCGCTCAAGCTCTAATCGGGCATCCCTTTAGGGTTCCGAT
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2049 GCGCTGATAGCGGTTTTCGCCCTTTCAGCTTTCAGGTCACGTTCTTAAAT
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[illegible]







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D3	479	ATTTCAGCTCCGGTTCCCAAGATCAAGCCAGATTACATGATCCCCCATGTTGTGCAAAA	4852
Q3	579	AGCGTTTAGCTCTCTTCGGTCTCCGATCGTTGTGTCAGAAATGAAGTTGGCCCGCAGTGTATC	5855
D3	485	AGCGTTTAGCTCTCTTCGGTCTCCGATCGTTGTGTCAGAAATGAAGTTGGCCCGCAGTGTATC	4912
Q3	585	ACTCATGGTTATGGCAGCATGTCATAAATCTCTTACTGTCTATGTCATGCCATCCGTAAAGATGCTT	5915
D3	491	ACTCATGGTTATGGCAGCATGTCATAAATCTCTTACTGTCTATGTCATGCCATCCGTAAAGATGCTT	4972
Q3	591	TCTGTGACATGGTGGTACTCAACCAAGTCAATCTCTGAGATAGTGTATGGCGGACCGAG	5975
D3	497	TCTGTGACATGGTGGTACTCAACCAAGTCAATCTCTGAGATAGTGTATGGCGGACCGAG	5032
Q3	597	TTCCTTTGCGCGGCTCAATACGGGATTAATACCGCGCCACATAGCAGAACTTTAAAAAGT	6035
D3	503	TTCCTTTGCGCGGCTCAATACGGGATTAATACCGCGCCACATAGCAGAACTTTAAAAAGT	5092
Q3	503	GCTCATCATTTGGAAAAAGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTGGAG	6095
D3	509	GCTCATCATTTGGAAAAAGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTGGAG	5152
Q3	509	ATCCAGTTCGATGTAAACCACTCGTGCACCACTGATCTTCAGCATCTTTTACTTTTCAC	6155
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Q3	533	GGTTCCGGCGACATTTCCCGGAAAGTGCCACCTGACGTC	6375
D3	539	GGTTCCGGCGACATTTCCCGGAAAGTGCCACCTGACGTC	5432
RECU			
LCU			
DEU			
VERS			
SCHE			
REFE			
CU			
TC			
FRAT			
ORIG			

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Best Local Similarity	88.9%	Pred. No. 0			
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DB	1256	GGGCTCTATGGCTTCTGAGCGGAAAGAACACAGCTGGGGTCTTAGGGGGTATCC			1313
QY	1810	GCCCTGTAGCGGGGCATTAAAGCGCGGGGTGTGGTGTTCACGCGACGCGTAC			1856
DB	1316	GCCCTGTAGCGGGCAATTAAAGCGCGGGGTGTGGTGTTCACGCGACGCGTAC			1359
QY	1870	ACTTGCAGCGCCCTAGGCGCGGCTCTTTCGCTTCTTCCCTTCTCTTCTCGC			1929
DB	1376	ACTTGCAGCGCCCTAGGCGCGGCTCTTTCGCTTCTTCCCTTCTCTTCTCGC			1435
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DB	1436	CGCGGGCTTTCCCGCTCAAGCTCTAAATCGGGGATCCCTTTAGGGTTCGGATT			1493
QY	1989	TTTACGCGACCTCGACCCCAAAACATTGATTAGGGTGATGGTTCAGTAGTGG			2048
DB	1496	TTTACGCGACCTCGACCCCAAAACATTGATTAGGGTGATGGTTCAGTAGTGG			1555
QY	2049	GCCCTGATAGAGGGTTTTTTCGCTTCTTGAAGTTGGAGTCAAGTTCCTTAATAG			2108
DB	1556	GCCCTGATAGAGGGTTTTTTCGCTTCTTGAAGTTGGAGTCAAGTTCCTTAATAG			1635
QY	2109	CTTGTTCCAAACCTGGACACACACTCAACCTCTCTCGGTCTATTCTTTTGATT			2168
DB	1616	CTTGTTCCAAACCTGGAAACAACACTCAACCTCTCTCGGTCTATTCTTTTGATT			1735
QY	2169	GATTTTCCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTATAACAAAAATT			2228
DB	1676	GATTTTCCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTATAACAAAAATT			1735
QY	2229	GAATTAATCTGTGGAAATGCCCGGAGCTGTGTATATCCATTTTCGGATCTGATC			2288
DB	1736	GAATTAATCTGTGGAAATGCCCGGAGCTGTGTATATCCATTTTCGGATCTGATC			1734
QY	2289	GAGCGGAAAGAACCCAGCTGTGGATGTGTGTGATAGGGTGTGGAAGTCCC			2348
DB	1745	-----CTGTGGAAATGTGTGTGATAGGGTGTGGAAGTCCC			1757
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|||||CGCGAGGATCTCGTGTGACCCATGCGGATGCTCTTGGCCGAATATCATGTGGAA 3275  
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QY 4416 AGCGGTTTCGGTATTTGGGCGCTCTTCGCTTCTCTGCTCACTGACTCGCTGG  
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DB	120f		
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QY	131f	AACTCAAGTTAAGGATTTTGGTTCATGAGATTATCAAAAAAGGATCTTCACTAGATCCCT	5315
DB	138f		
QY	137f	CAAGTTACCAATGCTTAATCAGTGAAGGACCTATCTCAGCCATCTGTCTATTTTCGTTTCATC	5435
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DB	150f		
QY	149f	CCCGAGTGTCTCAATGATATACGGCGAGACCCACGCTCACCGGCTCCAGATTATCAGCAAT	5555
DB	156f		
QY	155f	AAACCCAGCAGCCGAAAGGGCCGAGCCGAGAAGTGGTCTTGCAACTTTATCCCGCTCCAT	5615
DB	162f		
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DB	168f		
QY	167f	CAAGTGTGTGCCAATGCTACAGGCATCGTGGTGTCTACGCTCGTCTGTTTGGTATGGCTTC	5735
DB	174f		
QY	173f	ATTACAGCTCCGGTTTCCCAAAGATCAAGCCGAGTTACATGATCCCCCATGTTGTGCAAAAA	5795
DB	180f		
QY	179f	AGCGGTTAGTCTCTTTCGGTCTCCCGATCGTTGTGAGAAGTAAGTTGGCGCGCAGTTTATC	5855
DB	186f		
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DB	192f		
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DB	198f		
QY	197f	TTGCTCTTTCGCCGGGCTCAATAACGGGATAATACCGCGCCACATAGCAGAACTTTAAAGT	6035
DB	204f		

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Qy	6096	ATTCAGTTTCGATGTAACCCACTCGTGACACCAACTGATCTTCAGCATCTTTTAC	6155	TTTACG
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Qy	6216	GACACGGAAATGTTGAATACTCATACTCTCTCTCTTTTCAATATTTTGAAGCAT	6275	TTTACG
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Db	5347	GGGTATTGTCTCATGCGCGATACATATTTGAATGTATTTAGAAAATAAACA	5406	TTTACG
Qy	6336	GGTTCCGCGACATTTTCCCCGAAAAGTGCCACCTGACGTC	6375	
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RESULT 6	BD195386	5446 bp	DNA	linear	PATENT	JP 2002-514061-A
LOCUS	BD195386					
DEFINITION	Composition and methods for administering Pneumococcal DNA					
ACCESSION	BD195386					
VERSION	BD195386.1	GI:33005156				
KEYWORDS	JP 2002514061-A/3.					
SOURCE	unidentified					
ORGANISM	unidentified.					
REFERENCE	1 (bases 1 to 5446)					
AUTHORS	Briles,D.E., McDaniel,L.S. and Curtiel,D.T.					
TITLE	Composition and methods for administering Pneumococcal DNA					
JOURNAL	Patent: JP 2002514061-A 3 14-MAY-2002;					
	UNIVERSITY OF ALABAMA AT BIRMINGHAM					
COMMENT	OS Unidentified					

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	Query Match	56.1%	Score 3578.4;	DB 6;	Length 5446;
	Best Local Similarity	88.9%	Pred. No. 0;		
	Matches 4141;	Conservative 0;	Mismatches 16;	Indels 503;	
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QY	1810	GCCCTGTAGCGGCGCATTAAGCGCGGGGTGTGGTGTACGCGACGCGTGAC	1810	1869	
DB	1316	GCCCTGTAGCGGCGCATTAAGCGCGGGGTGTGGTGTACGCGACGCGTGAC	1316	1375	
OY	1870	ACTTGCCACGCGCCCTAGCGCGCGCTCTTTTCGCTTTCTTCCTTCTCTTCTGCG	1870	1928	



Qy	056	TATTTGCAGCGCTTAATAATGGGTTACAAATAAAAGCAATAGCATCACAAATTTTCACAAATAAAGC	4115
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Qy	176	CTGTATACCGGTGCAGACCTCTAGCTTAGAGCTTGGCGTAAATCATGGTCACTAGCTGTTTCTCTGT	4235
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Qy	236	GTTGAAATTTGTTATCCCGCTCACAATTTCCACAACAACATACGAGCCGGAAGCATAAAGTGTAA	4295
Db	307	GTTGAAATTTGTTATCCCGCTCACAATTTCCACAACAACATACGAGCCGGAAGCATAAAGTGTAA	3366
Qy	296	AGCTGTGGGTGCTTAATAGTGAGCTTAATCTCAATTAATTGGTTGGGTCTCATCTGCCCGC	4355
Db	367	AGCTGTGGGTGCTTAATAGTGAGCTTAATCTCAATTAATTGGTTGGGTCTCATCTGCCCGC	3426
Qy	356	TTTTTCCAGTTCGGGAAACCTGTCTGTCAGCTGCATTAATGAATCGGCCAAACGCGCGCGGAG	4415
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Qy	141	AGCGGTGTTTGGTATTGGGCGCTCTTCCGCTTCTCTCGCTCACTGACTCGCTGCGCTCGGT	4475
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Qy	147	CTTTCCGCTGCGGAGCGGTATCAGCTCATCTCAAGCGCGTAAATACGGTTATTCACAGA	4535
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QY	5436	CATAGTTGC	CTGACTCCCGCTCGTGTAGATAAATAAGGATACGGAGGGCTTAACC	CAATTC	5495
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QY	5736	ATTCAGCTC	CGGTGCCCAAGCATCAGGCGAGTTACATGATCCCCCATGTTGTG	CAATTC	5795
DB	4807	ATTCAGCTC	CGGTGCCCAAGCATCAGGCGAGTTACATGATCCCCCATGTTGTG	CAATTC	4866
QY	5796	AGCGGTTAG	CTCCTCCGATCGTTGTTCAGAAAGTAAGTTGGCCCGCAGT	CAATTC	5853
DB	4867	AGCGGTTAG	CTCCTCCGATCGTTGTTCAGAAAGTAAGTTGGCCCGCAGT	CAATTC	4926
QY	5856	ACTCATGGT	TATGCGAGCATGTCATAATCTCTTATCTGTCTATGCGATCCCGTAG	CAATTC	5913
DB	4927	ACTCATGGT	TATGCGAGCATGTCATAATCTCTTATCTGTCTATGCGATCCCGTAG	CAATTC	4986
QY	5916	TTCTGTGAC	TGCTGACTCTCAACCAAGTCAATCTGAGATAGTGTATGGGG	CAATTC	5973
DB	4987	TTCTGTGAC	TGCTGACTCTCAACCAAGTCAATCTGAGATAGTGTATGGGG	CAATTC	5046
QY	5976	TTGCTCTTG	CCCGGCTCAATACGGGATAATACCGCGCCACATAGCAGAACTTT	CAATTC	6033
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 AUTHORS Vekris,A., Masse,K. and Arveiler,B.  
 TITLE Eucaryotic cells transfection reporter vector  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 6109)  
 AUTHORS Vekris,A., Masse,K. and Arveiler,B.  
 TITLE Direct Submission  
 JOURNAL Submitted (24-FEB-1997) Lab. Pathologie Molculaire et T  
 Genique, Universite de Bordeaux II, 146, rue Leo Saignat  
 33076, France  
 COMMENT This sequence has been compiled from information in the  
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 at +33 5 57571010, extension 6476 or E-mail vekris@bor  
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 QY 2049 GCGCTGATAGCGGTTTTTTCGCGCTTTGAGCTTGGAGTCCACGTTCTTTAATAG  
 Db 2219 GCGCTGATAGCGGTTTTTTCGCGCTTTGAGCTTGGAGTCCACGTTCTTTAATAG

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DB	1931	TCAGCGAGGGCGCCCGGTTCTTTTGTCAAGACCGACTGTTCGGTGCCTGAAATGAA	2990	DB	3661	-----ACG	3669
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VE 3:	7:207724.1	GI:15422408			
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SC 5:	synthetic construct				
ER 6:	synthetic construct				
RT 7:	artificial sequences.				
AT 8:					
TI 9:	Jack, J.H., Whitney, M., Cubitt, A.B. and Pollok, B.A.				
CO 10:	Methods of protein destabilization and uses thereof				
FE 11:	Inventor: WO 0157242-A 22 09-AUG-2001;				
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SE 15:	Similarity	88.9%;	Pred. No. 0;		
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DE 18:	GGGCTCTATGGCTTCTGAGCGGAAAGAACACAGCTGGGCTCTAGGGGGTATCCCCACGC	2049			
QY 19:	GCCTGTAGCGGGCATTAAGCGGGCGGGTGTGGTGTACCGCGACGCTGACCGGTAC	1869			
DE 20:	GCCCTGTAGCGGGCATTAAGCGCGCGGGTGTGGTGTACCGCGACGCTGACCGGTAC	2109			
QY 21:	ACTTGCACGCGCCTAGCGCGCGCTCTTTCGGTTCCTCCCTTCTCTTCTCGCCAGCTT	1929			
DE 22:	ACTTGCACGCGCGCTAGCGCGCGCTCTTTCGGTTCCTCCCTTCTCTTCTCGCCAGCTT	2169			
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DE 24:	CGCGGGCTTTCGCCGTCAAGCTCTAAATCGGGGCGCGGCTTCGATTTAGTTC	2229			
QY 25:	TTTACGCGCATCTGACACCCCAAAAACCTTGATTTAGGGTGATGGTTCAGTATGGGCGATC	2048			
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Conservative	0	Mismatches	16	Indels	503	Gaps	5
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RESULT 13	EVPCMVPA1	6331 bp	DNA	linear	SYN
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DEFINITION	X96612				
ACCESSION	X96612.1	GI:1228975			
VERSION	expression vector; protein A.				
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1				
AUTHORS	Uetz, P. and Zeller, R.				
TITLE	Vectors for expression of protein-A-tagged proteins in v				
JOURNAL	Anal. Biochem.	237 (1),	161-163	(1996)	
MEDLINE	96299083				
PUBMED	8660557				
REFERENCE	2	(bases 1 to 6331)			
AUTHORS	Uetz, P.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (07-MAR-1996) P.H. Uetz, EMBL, Differentiation				
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414.; Conservative 0; Mismatches 16; Indels 503; Gaps 5;

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3.6511.1 synthetic construct
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REFERENCE
AUTHORS Uetz,P. and Zeller,R.
TITLE Vectors for expression of protein-A-tagged proteins in vertebrate
cells
JOURNAL Anal. Biochem. 237 (1), 161-163 (1996)
MEDLINE 9629083
PUBMED 8660557
REFERENCE 2 (bases 1 to 6333)
AUTHORS Uetz,P.H.
TITLE Direct Submission
JOURNAL Submitted (07-MAR-1996) P.H. Uetz, EMBL, Differentiation Biology
Meyerhofstr. 1, Heidelberg, 69117, FRG
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Search completed: July 15, 2004, 15:25:47  
Job time : 23848 secs



GenCore version 5.1.6  
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OM n: : - nucleic search, using sw model

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Run :
July 15, 2004, 07:08:15 ; Search time 2170 Seconds
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**Title: US-10-668-496-2**

Page 1096 6375

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Gapop 10.0 , Gapext 1.0

Sp. 2. 3373863 seqs, 2124099041 residues

To a per of hits satisfying chosen parameters: 6747726

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3 56 : length: 0

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3 36 : length: 2000000000
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PC: 0
ASS: 0
Minimum Match: 0%
Maximum Match: 100%
Listing first 45 summaries

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5: geneseq2001b.*
6: geneseq2002s.*
7: geneseq2003a.*
8: geneseq2003b.*
9: geneseq2003c.*
10: geneseq2004s.*
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1.  $\hat{y}_i$  is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution.

## SUMMARIES

Ref	N	Accession	Query Match	Length	DB	ID	Description	
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	380	2	56.2	5653	2	AAH02998	RSV tar R	Aah02998
	380	2	56.2	5900	6	ABQ81146	Expressio	Abq81146
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	378	3	56.1	5431	6	ABN86685	Nucleotid	Abn86685
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	378	3	56.1	6085	7	AAD56213	Human AB-	Aad56213
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## ALIGNMENTS

## RESULT 1

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14-OCT-2003 (first entry)  
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pcDNA3.1(+)-Edg5 nucleotide sequence SEQ ID NO:4.  
XX  
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Human; sphingosine 1 phosphate receptor; EDG5; CAM; identificat  
XX  
XX  
endothelial differentiation gene 5; constitutively active mutant; 100%;  
XX  
ds.

31 BP; 1408 A; 1759 C; 1660 G; 1604 T; 0 U; 0 Other;

56.2%; Score 3581.4; DB 8; Length 6431;  
 ilarity 88.9%; Pred. No. 0;  
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 QY 393 GATTCCACCGCCCTTCTATGAAAGGTTGGGCTTCGGAAATCGTTTTCGGGACGCGCGC 3996  
 DL 399 GATTCCACCGCCCTTCTATGAAAGGTTGGGCTTCGGAAATCGTTTTCGGGACGCGCGC 4055  
 QY 399 TGATGATCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCCGCCCAACCCCACTTGTT 4056  
 DL 405 TGATGATCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCCGCCCAACCCCACTTGTT 4115  
 QY 405 ATTGCAGCTTATAATGGTTACAATAAAGCAATAGCATCACAAATTTCAAAATAAGCA 4116  
 DL 411 ATTGCAGCTTATAATGGTTACAATAAAGCAATAGCATCACAAATTTCAAAATAAGCA 4175  
 QY 411 TTTTTTCACTGCATCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTC 4176  
 DL 417 TTTTTTCACTGCATCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTATCATGTC 4235  
 QY 417 TGTATACGCTGCACCTCTAGCTAGAGCTTGGCGTAATCATGTGCTATGCTGTTTCTCTGTG 4236  
 DL 423 TGTATACGCTGCACCTCTAGCTAGAGCTTGGCGTAATCATGTGCTATGCTGTTTCTCTGTG 4295  
 QY 423 TGAATTTGTTATCCGCTCACAAATTCACACAAATAGCAGCCGGAAGCATAAAGTGTA 4296  
 DL 429 TGAATTTGTTATCCGCTCACAAATTCACACAAATAGCAGCCGGAAGCATAAAGTGTA 4355  
 QY 429 GCTGGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTCGTTGCGCTCACTGCCGCT 4356  
 DL 435 GCTGGGGTGCCTTAATGAGTGAGCTAACTCACATTAATTCGTTGCGCTCACTGCCGCT 4415  
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 QY 471 CCGCTGGAGACTCCCTCGTGGCTCTCTGTTCCGACCTCGGCTTACGGATACCTG 4776  
 DL 477 CCGCTGGAGACTCCCTCGTGGCTCTCTGTTCCGACCTCGGCTTACGGATACCTG 4835  
 QY 477 CCGCTCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAAGCTGTAGTATCTC 4836  
 DL 483 CCGCTCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAAGCTGTAGTATCTC 4895  
 QY 483 AGTTCCGTGTAGTGTGCTTCCAGCTGGCTGTGTGCAAGAACCCCGTTTACGCC 4896  
 DL 489 AGTTCCGTGTAGTGTGCTTCCAGCTGGCTGTGTGCAAGAACCCCGTTTACGCC 4955

QY 4897 GACCGCTGCGCGCTTATCCGTTAACTATCGTCTTGTAGTCCAAACCCGTTAAGACAC 4956  
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 QY 5197 AAAGGATCTCAAGAGATCCTTTTGATCTTTTCTACGGGGTCTCAGCGTCAGTGC 5256  
 DL 5253 AAAGGATCTCAAGAGATCCTTTTGATCTTTTCTACGGGGTCTCAGCGTCAGTGC 5312  
 QY 5257 AACTCAGTTAAGGATTTTGGTTCATGAGATTAATCAAAAAGGATCTTACCTAC 5316  
 DL 5313 AACTCAGTTAAGGATTTTGGTTCATGAGATTAATCAAAAAGGATCTTACCTAC 5372  
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 QY 5377 AGTTACCAATGCTTAATCAGTGAGGACCTATCTCAGCGATCTGTCTATTTTCT 5436  
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 DL 5673 CAGTCTATTAAATTTGTTCCGGGAGCTAGAGTAAGTGTTCGCCAGTTAATAGT 5722  
 QY 5677 AAGTTGTTGCCATTCCTACAGCATCGTGTCTCAGCTCGTCTGTTTGTATC 5726  
 DL 5733 AAGTTGTTGCCATTCCTACAGCATCGTGTGTCTCAGCTCGTCTGTTTGTATC 5792  
 QY 5737 TACAGTCTCGGTTTCCAAACGATCAAGCGAGTTACATGATCCCCCATTTGTGC 5796  
 DL 5793 TACAGTCTCGGTTTCCAAACGATCAAGCGAGTTACATGATCCCCCATTTGTGC 5852  
 QY 5797 GCGGTTAGTCTCTCGTCTCGATCGTGTGTCAGAGTAAGTTGCGCCGAGTC 5856  
 DL 5853 GCGGTTAGTCTCTCGTCTCGATCGTGTGTCAGAGTAAGTTGCGCCGAGTC 5912  
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 QY 5977 TGCTCTTCCCGCGCTCAATA CGGGATAATACCGGCCCATAGAGAACTTTA 6036

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 CATATGTGAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTGAGA 6152  
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 CAGTTGATGTAAACCACTCGTGACCCCACTGATCTTACGATCTTTACTTTACCC 6212  
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 TTATTGCTCATGAGCGGATACATATTTGAATGTTATGAAATATTTAGAAATATAA 6392  
 TCGCGCACATTTCCCGGAAAGTGCCACCTGACGTC 6375  
 TCGCGCACATTTCCCGGAAAGTGCCACCTGACGTC 6431

standard; DNA; 7648 BP.

(first entry)

Ub DNA.

protease function; protein metabolism; toxicology;  
 y; vector; db.

Al.

; 2000DE-01064343.

; 2000DE-01064343.

LEN P.  
 NER C.

Wenner C;

97721/55.

intracellular protein metabolism using new nucleic acid  
 comprising multiple ubiquitin coding sections and a selection

Fig 7; 16pp; German.

ion describes a novel nucleic acid (I), comprising at least  
 in coding section and a selection marker fixed at a separate  
 on the ubiquitin coding section. The invention is used to  
 protease function in protein metabolism. This is useful in  
 and general cell biology. The invention provides a method that  
 quicker, and more reproducible than prior art methods where  
 in is only transiently expressed. This sequence represents the  
 Ub encoding DNA is used in the method of the invention

SQ Sequence 7648 BP; 1850 A; 2036 C; 1947 G; 1815 T; 0 U; 0 Other;  
 Query Match 56.2%; Score 3581.4; DB 4; Length 7648;  
 Best Local Similarity 88.9%; Pred. No. 0;  
 Matches 4143; Conservative 0; Mismatches 11; Indels 505;  
 QY 1750 GAGCTCCAGCTTTTCTGAGGGGAAAGAACCCAGCTTGGGGCTCTAGGGGGTATCC  
 Db 3462 GGGCTCTATGGCTTTCTGAGGCGAAAGAACCCAGCTTGGGGCTCTAGGGGGTATCC  
 QY 1810 GCCCTGTAGCGCGCATTAAGCGCGGGGTGTGGTGTACGCGCAGCGTGAC  
 Db 3522 GCCCTGTAGCGCGCATTAAGCGCGGGGTGTGGTGTACGCGCAGCGTGAC  
 QY 1870 ACTTGCAGCGCCCTAGCGCGGCTCTTTCCGCTTTCTTCCCTTCTCTCTCGC  
 Db 3582 ACTTGCAGCGCCCTAGCGCGGCTCTTTCCGCTTTCTTCCCTTCTCTCTCGC  
 QY 1930 CGCGGGCTTTCCCGCTCAAGCTCTAAATC- -GGGGCTCCCTTTAGGGTTCCGANT  
 Db 3642 CGCGGGCTTTCCCGCTCAAGCTCTAAATC- -GGGGCTCCCTTTAGGGTTCCGANT  
 QY 1989 TTTACGGCACTCGACCCCAAAAACTTTGATTAGGGTGTAGTGTACAGTAGTGG  
 Db 3702 TTTACGGCACTCGACCCCAAAAACTTTGATTAGGGTGTAGTGTACAGTAGTGG  
 QY 2049 GCCCTGTAGACGGTTTTTTCGCTTTGACGCTTGGAGTCCAGCTTTTAAATAG  
 Db 3762 GCCCTGTAGACGGTTTTTTCGCTTTGACGCTTGGAGTCCAGCTTTTAAATAG  
 QY 2109 CTGTGTTCCAAACTGGAACAACACTCAACCTCTATCTCGGTCTATTCTTTTGTATTT  
 Db 3822 CTGTGTTCCAAACTGGAACAACACTCAACCTCTATCTCGGTCTATTCTTTTGTATTT  
 QY 2169 GATTTTGCAGTTTTCGGCTATTGGTTTAAAAAATGAGCTGATTTAAACAAAAATT  
 Db 3882 GATTTTGCAGTTTTCGGCTATTGGTTTAAAAAATGAGCTGATTTAAACAAAAATT  
 QY 2229 GAATTAATCTGTGGATGCGCGGAGCTTGATATCCATTTTCGGATCTGATC  
 Db 3942 GAATTAATT- - - - -  
 QY 2289 GAGCGGAAAGAACAGCTGTGGAATGTGTGCTAGTTAGGTGTGAAAGTCCC  
 Db 3951 - - - - -CTGTGGAAATGTGTGCTAGTTAGGTGTGAAAGTCCC  
 QY 2349 CCCAGCAGGCGAGGATGCAAAAGCATGCAATCTCAATTAGTCAGCAACAGAGT  
 Db 3994 CCCAGCAGGCGAGGATGCAAAAGCATGCAATCTCAATTAGTCAGCAACAGAGT  
 QY 2409 AGTCCCGAGGCTCCCGAGGCGAGGATGCAAAAGCATGCAATCTCAATTAGT  
 Db 4054 AGTCCCGAGGCTCCCGAGGCGAGGATGCAAAAGCATGCAATCTCAATTAGT  
 QY 2469 CCATAGTCCCGCCCTTAACCTCCGCGCCATCCCGCCCTAACTCCGCGCCAGTTCCG  
 Db 4114 CCATAGTCCCGCCCTTAACCTCCGCGCCATCCCGCCCTAACTCCGCGCCAGTTCCG  
 QY 2529 CTCGCGCCCATGCTGATTAATTTTATTTTATTTATGAGAGGCGAGGCGCCCT  
 Db 4174 CTCGCGCCCATGCTGATTAATTTTATTTTATTTATGAGAGGCGAGGCGCCCT  
 QY 2589 CTGAGCTATTCCAGAGTAGTAGGAGGCTTTTGGAGGCTTAGGCTTTTGGCA  
 Db 4234 CTGAGCTATTCCAGAGTAGTAGGAGGCTTTTGGAGGCTTAGGCTTTTGGCA  
 QY 2649 - - - - -GATCAAGAGACAGGATGAGGAT  
 Db 4294 TCCCGGAGCTTGTATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGGAT  
 QY 2677 GCATGATTAACAGATGAGTTCAGCCAGGTTCTCCGCGCGCTTGGGTGAGA  
 Db 4354 GCATGATTAACAGATGAGTTCAGCCAGGTTCTCCGCGCGCTTGGGTGAGA

QY 273 TCGGCTATCATCGGGCAACAGACAATCGGCTGTCTGATGCGCGCTGTTCGGCTGT 2796  
 D# 1413 TCGGCTATGACTGGGCAACAGACAATCGGCTGTCTGATGCGCGCTGTTCGGCTGT 4473  
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 D# 1474 CAGCGAGGGGCGCGGCTCTTTTGTCAAGACCGACCTGTCCGGTGCCTGAATGAAC 4533  
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 D# 1534 TCGAAGACGAGGCGCGGCTATCGTGGCTGGCCACGACGGGCTTCCTTGGCGAGCTG 4593  
 QY 2917 TCGCTGACCTGTCTCATGAGCGGGAAGGAGCTGGCTGTATTTGGCGAAGTGC CGGGC 2976  
 D# 1594 TCGCTGACCTGTCTCATGAGCGGGAAGGAGCTGGCTGTATTTGGCGAAGTGC CGGGC 4653  
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 D# 1654 AGATCTCTGTGATCATCTCACTTGTCTTCCGCGAGAAAGTATCCATCATGGCTGATGCAA 4713  
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 D# 1894 AGGGCGAGGATCTCGCTGCTGACCCATGGGATGCTTGTCCGAAATATCATGGTGGAAA 4953  
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 D# 1954 ATGGCGCTTTTCTGATATCATGACTGTGGCGCGCTGGGTGGCGGACCGTATCAGG 5013  
 QY 3337 ACATAGCTTGGCTACCGCTGATATTCGAGAGCTTCGCGCGGATGGCTGACCGCT 3396  
 D# 3017 ACATAGCTTGGCTACCGCTGATATTCGAGAGCTTCGCGCGGATGGCTGACCGCT 5073  
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 D# 3074 TCGCTCGCTTTTACGGTATCGCGCTCCCGATTCGACGCGCATCGCTTCTATCGCTTC 5133  
 QY 3457 TCGACGAGTTCTTCTGAGCGGAGCTCTGGGTTTGAATAAGACGACGACGCGCCAA 3516  
 D# 3134 TCGACGAGTTCTTCTGAGCGGAGCTCTGGGTTTGAATAAGACGACGACGCGCCAA 5193  
 QY 3517 CTGCGCATCAGAGATTCGATTCACCGCGGCTTCTATGAAAGTTGGGCTTCGGAAT 3576  
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 QY 3577 CGTTTTCCGGGACGCGGCTGATGATCTCTCCAGCGGGGATCTCATGTGGAGTTCTT 3636  
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RESULT 3
AA020298
ID AAT02998 standard; DNA; 5653 BP.
XX AC AAT02998;
XX DT 24-MAR-1996 (first entry)
XX DE RSV tar Rev M10 expression plasmid pRSVtarRevM10.
XX KW Plasmid pRSVtarRevM10; particle-mediated gene transfer; cyclic;
KW particle acceleration; HIV virus infection; gene therapy; ss.
XX OS Synthetic.
XX FH Key Location/Qualifiers
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FT /note= "pBR322 vector sequence"
FT enhancer 37..610
FT /tag= b
FT /note= "RSV enhancer"
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FT /tag= c
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FT /note= "HIV promoter tat responsive element"
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FT /tag= d
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FT misc_feature 3459..5653
FT /tag= i
FT /note= "plasmid pUC ori/amp sequence"
XX
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[illegible]

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andard; DNA; 6216 BP.

/ASK8-SmGST3 DNA.

**mangoni.**

: 97WO-US003977.

96US-0013321P.

70644/43.

p 7a; 57pp; English.

as been developed comprising a non-infectious, non-integrating DNA encoding *Schistosoma mansoni* glutathione S-transferase. The vector comprises a plasmid encoding a protein, polypeptide or ch is operably linked to a promoter. The present sequence

SQ Sequence 6216 BP; 1428 A; 1624 C; 1627 G; 1537 T; 0 U; 0 Other;  
Query Match 56.1%; Score 3578.6; DB 2; Length 6216;  
Best Local Similarity 88.6%; Pred. No. 0;  
Matches 4157; Conservative 0; Mismatches 64; Indels 470;

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 1991 GCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGTACCGCGCAGCGTGAC  
 |||

Qy 1930 CGCCGGCTTCCCGTCAAGCTCTAAATCGGGC - TCCTTTAGGGTTCGGATT  
 |||||  
 Ph 2111 CGCCGATTTTCCCGCTCAAGCTCTAAATCGGGC - TCCTTTAGGGTTCGGATT  
 |||||

QY 2049 GCCTGTAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAG

QY 2169 GATTTTGGCGATTTCGGGCTATTGGTTAAAAAATGAGCTGATTTTACAAAAATT

DD	2411	GAATTTTAAACAAATATTAACGTTTACAATTTAAATATTGCTTATACAAATCT
QY	2262	TATCCATTTTCGGATCTGATCAGCACTGAGCGGGAAGAACCCAG-----CTGTGG

DB	QY
2531	2377
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Db	2651	TATGCAAGCATGTCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCCTAACTCC
Qy	2497	CCCGCCCTAACTCCGCCCAGTTCGGCCCATTTCTCGCCCCCATGGCTGACTAAT

Db	2771	TATTTATG	CAGAGG	CGCGCT	CTGAGCT	TATTC	GAA	GTA	GTAGT
Qy	2617	CTTTTTTT	TGGAGG	CGCTAG	CTTTT	TGCA	A	A	GATC-----

283: CTTTTTGGAGGCTAGGCTTTTGGCAAAAGCTCCCGGAGCTTGGATATCCATTTTCGG 2890  
 264: ---GATCAAGAGACAGGATGAGATCGTTTCATGATTGAACAAGATGGATTGCACGC 2704  
 289: ATCTGATCAAGAGACAGGATGAGATCGTTTCATGATTGAACAAGATGGATTGCACGC 2950  
 370: AGGTTCTCCGGCGCTTGGGTGAGAGGCTATTCCGCTATGACTGGGCAACAAGACAAT 2764  
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 313: GTTGGCCACGACGGGCGTTCCTTGGCGAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAG 3190  
 294: GGAATGCTGCTATTGGGCGAGTGTGCGGCGAGGATCTCTGTCTATCTCACCTGCTCC 3004  
 319: GGAATGCTGCTATTGGGCGAGTGTGCGGCGAGGATCTCTGTCTATCTCACCTGCTCC 3250  
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 331: TACTGCTCCATTCGACCAACAAGCGAAACATGCGATCGAGCGAGCGTACTCGGATGGA 3370  
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 373: GGTTCGAAATGACCGACGAGCGGCGCAACCTGCGCATCAGAGATTCGATTCACC 3771  
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 360: CTCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCCAACCTTAGGGGAGGCTAACTGAA 3664  
 377: ----- 3771  
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 3772: -----ACGAGATTTCGATTCCACCGCGGCTTCTATG 3809  
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 4085: GCAATAGCATCAAAATTTTCAAAATAAAGCATTTTTTTCACCTGCACTTAGTT 4144  
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 4145: TGTCCAAATCAATGATATCTTATCATGTCTGTATACCGTCGACCTCTAGCT 4204  
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 4205: TGGGTAATCATGCTCATAGCTGTTTCTGTCGTAATGTTATCGCTCAGAA 4264  
 4046: TGGGTAATCATGCTCATAGCTGTTTCTGTCGTAATGTTATCCGCTCAGAA 4105  
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 4346: ACTCAAGCGGTAATACGTTATCCACAGAAATCAGGGGATTAACGAGGAAAGA 4405  
 4565: GAGCAAAAGCGCAGCAAAAGGCGAGCAACCGGTAAAGGCGCGTTCGTCGGCT 4624  
 4406: GAGCAAAAGCGCAGCAAAAGGCGAGCAACCGGTAAAGGCGCGTTCGTCGGCT 4465  
 4625: ATAGGCTCGCGCCCTCGACGAGCATCAAAAATTCGACGCTCAAGTCAGAGGT 4684  
 4466: ATAGGCTCGCGCCCTCGACGAGCATCAAAAATTCGACGCTCAAGTCAGAGGT 4525  
 4685: ACCGACAGGACTATAAGATACGAGGCGTTTCCCTCGGAAAGCTCCCTCGTGC 4744  
 4526: ACCGACAGGACTATAAGATACGAGGCGTTTCCCTCGGAAAGCTCCCTCGTGC 4585  
 4745: CTGTTCCGACCTCGGCTTACGGATACCTTCGCGCTTTCTCCCTTCGGGAA 4804  
 4586: CTGTTCCGACCTCGGCTTACGGATACCTTCGCGCTTTCTCCCTTCGGGAA 4645

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ATCTCAGCAGATCTGTCTATTTGGTCTATCCATAGTTGCTGACTCCCGCTCGTGA 5305  
ACTAGATACGGGAGGCTTACCATCTGGCCCGCTGCTGCAATGATACCGGAGACC 5524  
ACTAGATACGGGAGGCTTACCATCTGGCCCGCTGCTGCAATGATACCGGAGACC 5365  
CGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCGGAGGCGGAGCGCA 5584  
CGCTCACCGGCTCCAGATTTATCAGCAATAAACCCAGCCAGCGGAGGCGGAGCGCA 5425  
AGTGGTCTGCAAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAGCTA 5644  
AGTGGTCTGCAAACTTTATCCGCTCCATCCAGTCTATTAATTTGTCGGGAAGCTA 5485  
GTAAGTGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTTGCTACAGGATCG 5704  
GTAAGTGTTCGCCAGTTAATAGTTTGGCAACGTTGTTGCCATTTGCTACAGGATCG 5545  
GTGTCAAGCTCTGCTGTTGGTATGCGTTCAITTCAGCTCCGTTCCCAACGATCAAGGC 5764  
GTGTCAAGCTCTGCTGTTGGTATGCGTTCAITTCAGCTCCGTTCCCAACGATCAAGGC 5605  
GTTACATGATCCCGATGTTGGTGAAGAAAGCGGTTAGCTCCTTCGTTCCGATCG 5824  
GTTACATGATCCCGATGTTGGTGAAGAAAGCGGTTAGCTCCTTCGTTCCGATCG 5665  
GTCAAGATGAGTTGGCCGAGTGTATCACTCATGTTTATGCGCAGCACTGATTAATT 5884  
GTCAAGATGAGTTGGCCGAGTGTATCACTCATGTTTATGCGCAGCACTGATTAATT 5725

QY 5885 CTCTTACTGTGTCATCCATCCGTAAGATGCTTTTCTGTGATGTGGTGAATCTCA 5885  
Db 5726 CTCTTACTGTGTCATCCATCCGTAAGATGCTTTTCTGTGATGTGGTGAATCTCA 5726  
QY 5945 CATTTCTGAGAAATAGTGTATGCGGCGACCGAGTTGCTCTTGGCCCGGCTCAATAC 5945  
Db 5786 CATTTCTGAGAAATAGTGTATGCGGCGACCGAGTTGCTCTTGGCCCGGCTCAATAC 5786  
QY 6005 ATACCGCGCCACATAGCAGAACTTTTAAAGTGTCTCATATTTGGAAGAAAGTTCTT 6005  
Db 5846 ATACCGCGCCACATAGCAGAACTTTTAAAGTGTCTCATATTTGGAAGAAAGTTCTT 5846  
QY 6065 GAAATCTCTCAAGGATCTTACCGCTGTGAGATCCAGTTCCATGTAACCCACTC 6065  
Db 5906 GAAATCTCTCAAGGATCTTACCGCTGTGAGATCCAGTTCCATGTAACCCACTC 5906  
QY 6125 CCAACTGATCTTCAAGCATCTTTTACTTTTCAACGCGTTTCTGGGTGAGCAAAA 6125  
Db 5966 CCAACTGATCTTCAAGCATCTTTTACTTTTCAACGCGTTTCTGGGTGAGCAAAA 5966  
QY 6185 GGGAAATGCGCAAAAAGGAAATAGGGGACACCGAAATGTTGAATCTCA 6185  
Db 6026 GGGAAATGCGCAAAAAGGAAATAGGGGACACCGAAATGTTGAATCTCA 6026  
QY 6245 TCCTTTTTCAATATTTTGAAGCATTTTATCAGGTTATTTGCTCATGAGCGGAT 6245  
Db 6086 TCCTTTTTCAATATTTTGAAGCATTTTATCAGGTTATTTGCTCATGAGCGGAT 6086  
QY 6305 TTGAATGTTTATAGAAAAATAAACAATAGGGGTTCCGCGCACATTTCCCGGAA 6305  
Db 6146 TTGAATGTTTATAGAAAAATAAACAATAGGGGTTCCGCGCACATTTCCCGGAA 6146  
QY 6365 CACCTGAGCTC 6375  
Db 6206 CACCTGAGCTC 6216

RESULT 6

ABN86685  
ID ABN86685 standard; DNA; 5431 BP.  
XX AC ABN86685;  
XX DT 05-NOV-2002 (first entry)  
XX DE Nucleotide sequence of a pCDNA3 plasmid vector.  
XX KW Major histocompatibility complex; MHC; antigen presenting cell;  
XX KW antigen; cytostatic; virucide; gene therapy; CD8; vaccine; ther;  
XX KW cancer; viral infection; ds.  
XX OS Synthetic.  
XX FN WO200261113-A2.  
XX PD 08-AUG-2002.  
XX PP 01-FEB-2002; 2002WO-US0002598.  
XX PR 01-FEB-2001; 2001US-0265334P.  
XX PA (UWJO ) UNIV JOHNS HOPKINS.  
XX PI Wu T, Hung C;  
XX DR WPI; 2002-619261/66.  
XX PT Nucleic acid molecule encoding a fusion polypeptide that promot;  
XX PT processing via the Major Histocompatibility Complex class I pat;  
XX PT and/or promotes activity of an antigen presenting cell, useful;  
XX PT for cancer and viral infections.  
PS Claim 24; Page 22-23; 127pp; English.

Q1	Q2	Q3	Q4	Q5	Q6	Q7	Q8	Q9	Q10	Q11	Q12	Q13	Q14	Q15	Q16	Q17	Q18	Q19	Q20	Q21	Q22	Q23	Q24	Q25	Q26	Q27	Q28	Q29	Q30	Q31	Q32	Q33	Q34	Q35	Q36	Q37	Q38	Q39	Q40	Q41	Q42	Q43	Q44	Q45	Q46	Q47	Q48	Q49	Q50	Q51	Q52	Q53	Q54	Q55	Q56	Q57	Q58	Q59	Q60	Q61	Q62	Q63	Q64	Q65	Q66	Q67	Q68	Q69	Q70	Q71	Q72	Q73	Q74	Q75	Q76	Q77	Q78	Q79	Q80	Q81	Q82	Q83	Q84	Q85	Q86	Q87	Q88	Q89	Q90	Q91	Q92	Q93	Q94	Q95	Q96	Q97	Q98	Q99	Q100	Q101	Q102	Q103	Q104	Q105	Q106	Q107	Q108	Q109	Q110	Q111	Q112	Q113	Q114	Q115	Q116	Q117	Q118	Q119	Q120	Q121	Q122	Q123	Q124	Q125	Q126	Q127	Q128	Q129	Q130	Q131	Q132	Q133	Q134	Q135	Q136	Q137	Q138	Q139	Q140	Q141	Q142	Q143	Q144	Q145	Q146	Q147	Q148	Q149	Q150	Q151	Q152	Q153	Q154	Q155	Q156	Q157	Q158	Q159	Q160	Q161	Q162	Q163	Q164	Q165	Q166	Q167	Q168	Q169	Q170	Q171	Q172	Q173	Q174	Q175	Q176	Q177	Q178	Q179	Q180	Q181	Q182	Q183	Q184	Q185	Q186	Q187	Q188	Q189	Q190	Q191	Q192	Q193	Q194	Q195	Q196	Q197	Q198	Q199	Q200	Q201	Q202	Q203	Q204	Q205	Q206	Q207	Q208	Q209	Q210	Q211	Q212	Q213	Q214	Q215	Q216	Q217	Q218	Q219	Q220	Q221	Q222	Q223	Q224	Q225	Q226	Q227	Q228	Q229	Q230	Q231	Q232	Q233	Q234	Q235	Q236	Q237	Q238	Q239	Q240	Q241	Q242	Q243	Q244	Q245	Q246	Q247	Q248	Q249	Q250	Q251	Q252	Q253	Q254	Q255	Q256	Q257	Q258	Q259	Q260	Q261	Q262	Q263	Q264	Q265	Q266	Q267	Q268	Q269	Q270	Q271	Q272	Q273	Q274	Q275	Q276	Q277	Q278	Q279	Q280	Q281	Q282	Q283	Q284	Q285	Q286	Q287	Q288	Q289	Q290	Q291	Q292	Q293	Q294	Q295	Q296	Q297	Q298	Q299	Q300	Q301	Q302	Q303	Q304	Q305	Q306	Q307	Q308	Q309	Q310	Q311	Q312	Q313	Q314	Q315	Q316	Q317	Q318	Q319	Q320	Q321	Q322	Q323	Q324	Q325	Q326	Q327	Q328	Q329	Q330	Q331	Q332	Q333	Q334	Q335	Q336	Q337	Q338	Q339	Q340	Q341	Q342	Q343	Q344	Q345	Q346	Q347	Q348	Q349	Q350	Q351	Q352	Q353	Q354	Q355	Q356	Q357	Q358	Q359	Q360	Q361	Q362	Q363	Q364	Q365	Q366	Q367	Q368	Q369	Q370	Q371	Q372	Q373	Q374	Q375	Q376	Q377	Q378	Q379	Q380	Q381	Q382	Q383	Q384	Q385	Q386	Q387	Q388	Q389	Q390	Q391	Q392	Q393	Q394	Q395	Q396	Q397	Q398	Q399	Q400	Q401	Q402	Q403	Q404	Q405	Q406	Q407	Q408	Q409	Q410	Q411	Q412	Q413	Q414	Q415	Q416	Q417	Q418	Q419	Q420	Q421	Q422	Q423	Q424	Q425	Q426	Q427	Q428	Q429	Q430	Q431	Q432	Q433	Q434	Q435	Q436	Q437	Q438	Q439	Q440	Q441	Q442	Q443	Q444	Q445	Q446	Q447	Q448	Q449	Q450	Q451	Q452	Q453	Q454	Q455	Q456	Q457	Q458	Q459	Q460	Q461	Q462	Q463	Q464	Q465	Q466</
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[illegible]

1.86: standard; DNA; 5431 BP.

 $\Delta N = 104$  (first entry)

mid vector pcdNA3 nucleotide sequence SEQ ID NO:8.

eric fusion; translocation; antigenic; cytostatic; immunotherapy;  
the baby; cancer; tumour; gene; ds.

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030-085-A2.

ST-103.

PR. . . 03; 2003WO-US010235.

PR--(C2; 2002US-00115440.

C ) INIV JOHNS HOPKINS.

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203-377027/81.

[illegible]

New nucleic acid encoding a chimeric fusion or fusion polypeptide comprising a first domain with a translocation polypeptide, and a second domain with an antigen having at least one antigenic peptide, useful for treating cancer.

Disclosure; SEQ ID NO 8; 68pp; English.

The present invention describes a nucleic acid (I) encoding a fusion or fusion polypeptide comprising a first domain with a translocation polypeptide, and a second domain comprising an antigenic peptide, and a second domain comprising an antigenic peptide. Also described: (1) an expression vector comprising (I) operatively linked to a promoter and one or more regulatory elements that enhance expression of the nucleic acid in a cell; (2) a particle comprising (I) or the expression vector in a cell; (3) a cell that has been modified to comprise (I) or the expression vector; (4) a chimeric polypeptide comprising a first domain with a translocation polypeptide, and a second domain comprising an antigenic peptide; (5) a pharmaceutical composition capable of inducing or enhancing an antigen specific immune response comprising (I), expression vector, particle, cell, cell of the particle, or the chimeric polypeptide; and a carrier or excipient; (6) increasing an antigen specific immune response by administering a composition described above; (7) increasing the number of CD8<sup>+</sup> T cells specific for a selected desired antigen in a subject by administering a composition described above; and (8) inhibiting the growth of a tumor in a subject by administering the composition described above. (I) has cytostatic activity, and can be used in immunotherapy, and gene therapy. The nucleic acid (I), compositions and methods are useful for treating cancer. The present sequence represents a plasmid vector nucleic acid sequence which is used in the exemplification of the present invention.

Sequence 5431 BP; 1253 A; 1413 C; 1386 G; 1379 T; 0 U; 0 Other;

Query Match 56.1%; Score 3578.4; DB 9; Length 5431;  
Best Local Similarity 88.9%; Pred. No. 0;  
Matches 414; Conservative 0; Mismatches 16; Indels 503;

Qy	1750	GAGCTCAGCTTTTCTGAGCGCGAAGAACCACTCGGGCTCTAGGGGGTATCC	1503
Db	1241	GGGCTCTATGGCTTCTGAGCGGAAGAACCACTCGGGCTCTAGGGGGTATCC	1300
Qy	1810	GCCTGTAGCGGCGCATTAAGCGCGCGGGTGTGGTTTACCGCAGCGTGAC	1569
Db	1301	GCCTGTAGCGGCGCATTAAGCGCGCGGGTGTGGTTACGCGACGCGTGAC	1360
Qy	1870	ACTTGCAGCGCCCTAGCGCGCGCTCCTTTGCGTCTTTCCTTCCTTCTCGC	1528
Db	1361	ACTTGCAGCGCCCTAGCGCGCGCTCCTTTGCGTCTTTCCTTCCTTCTCGC	1420
Qy	1930	CGCGCGCTTTCGCCGTCAAGCTCTAAATCGGGC-TCCCTTTAGGGTTCGGATT	1568
Db	1421	CGCGCGCTTTCGCCGTCAAGCTCTAAATCGGGCATCCCTTTAGGGTTCGGATT	1460
Qy	1989	TTTACGCGCCTCGACCCCAAAAACTGANTAGGTGATGGTTCAGTAGTGG	2648
Db	1481	TTTACGCGCCTCGACCCCAAAAACTGANTAGGTGATGGTTCAGTAGTGG	1540
Qy	2049	GCCTCATAGACGGTTTTTCGCCCTTTGAGCTGGAGTCCACGCTCTTTAATAC	2108
Db	1541	GCCTCATAGACGGTTTTTCGCCCTTTGAGCTTGGAGTCCACGCTCTTTAATAC	1600
Qy	2109	CTTGTTCCAAATCGGAACAACCTCAACCTATCTCGGTCTATTCTTTTGATT	2168
Db	1601	CTTGTTCCAAATCGGAACAACCTCAACCTATCTCGGTCTATTCTTTTGATT	1660
Qy	2169	GATTTTCCGATTTCCGCCCTATTGGTTAAAAATGAGCTGATTTACAAAAAT	2228
Db	1661	GATTTTCCGATTTCCGCCCTATTGGTTAAAAATGAGCTGATTTACAAAAAT	1720
Qy	2229	GAATTAATTTCTGTGAATGCCCGGAGCTTGTAATCCATTTTCGGATCTGATC	2288
Db	1721	GAATTAATTTCTGTGAATGCCCGGAGCTTGTAATCCATTTTCGGATCTGATC	1729

203-377027/81.



D:	347:	AGCGGTTTGGCTATTGGGGCTCTTCCGGTTCCTCGCTCACTGACTCGCTGCGTCCGT	3531
Q:	447:	CGTTCCGCTGCGCGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGGTTATCCACAGA	4535
D:	353:	CGTTCCGCTGCGCGAGCGGTATCAGCTCACTCAAAAGGCGGTAAATACGGTTATCCACAGA	3591
Q:	453:	ATCAGGGGATTAACGACGGAAGAAAGATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCG	4595
D:	359:	ATCAGGGGATTAACGACGGAAGAAAGATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCG	3651
Q:	459:	TAAAAGGCGCGCTGCTGCGCTTTTCCATAGGCTCCGCCCCCTCGACGAGCATCACAA	4655
D:	365:	TAAAAGGCGCGCTGCTGCGCTTTTCCATAGGCTCCGCCCCCTCGACGAGCATCACAA	3711
Q:	465:	AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTT	4715
D:	371:	AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGTT	3771
Q:	471:	TCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCGCTCCGCTTACCGGATACCT	4775
D:	377:	TCCCTCGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCGCTCCGCTTACCGGATACCT	3831
Q:	477:	GTCGCGCTTTCTCCCTTCGGGAAAGCTGGCGCTTTCTCATGCTCAAGCTGTAGGTATCT	4835
D:	383:	GTCGCGCTTTCTCCCTTCGGGAAAGCTGGCGCTTTCTCATGCTCAAGCTGTAGGTATCT	3891
Q:	483:	CAGTTCGGTGTAGGTTCGCTTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCC	4895
D:	389:	CAGTTCGGTGTAGGTTCGCTTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCC	3951
Q:	489:	CGACCGCTGGCCTTATCCGGTAACCTATCGTCTTGAGTCCAAACCCGGTAAGACCACTT	4955
D:	395:	CGACCGCTGGCCTTATCCGGTAACCTATCGTCTTGAGTCCAAACCCGGTAAGACCACTT	4011
Q:	495:	ATCGCACTGGCAGCAGCCACTCGTAAACAGATTTAGCAGAGCAGGTATGTAGCGGTGC	5015
D:	401:	ATCGCACTGGCAGCAGCCACTCGTAAACAGATTTAGCAGAGCAGGTATGTAGCGGTGC	4071
Q:	501:	TACAGAGTTCCTGAAGTGTGGCTTAACCTACCGCTACCTAGAGAACAGTATTTGGTAT	5075
D:	407:	TACAGAGTTCCTGAAGTGTGGCTTAACCTACCGCTACCTAGAGAACAGTATTTGGTAT	4131
Q:	507:	CTCGCTCTGCTCAAGCCAGTACCTTCGGAAGAGTTGGTGTAGCTTTGATCCGCGAA	5135
D:	413:	CTCGCTCTGCTCAAGCCAGTACCTTCGGAAGAGTTGGTGTAGCTTTGATCCGCGAA	4191
Q:	513:	ACAAACACCGCTGGTAGCGGTGTTTTTTTGTTCGACGACAGATTACGCGCAGAA	5195
D:	419:	ACAAACACCGCTGGTAGCGGTGTTTTTTTGTTCGACGACAGATTACGCGCAGAA	4251
Q:	519:	AAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGA	5255
D:	425:	AAAGGATCTCAAGAGATCCTTTGATCTTTTCTACGGGCTCTGACGCTCAGTGGAAACGA	4311
Q:	525:	AAACTCAGTTAAGGATTTTGTCTAGATTATCAAAAGGATCTTACCTAGATCCT	5315
D:	431:	AAACTCAGTTAAGGATTTTGTCTAGATTATCAAAAGGATCTTACCTAGATCCT	4371
Q:	531:	TTTAAATTTAAATTTAAATTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGA	5375
D:	437:	TTTAAATTTAAATTTAAATTTAAATCAATCTAAAGTATATATGAGTAACTTGGTCTGA	4431
Q:	537:	CAGTTACCAATGCTTAATCAGTAGGCACTATCTCAGCGATCTGTCTATTTCTGTTCAATC	5435
D:	443:	CAGTTACCAATGCTTAATCAGTAGGCACTATCTCAGCGATCTGTCTATTTCTGTTCAATC	4491
Q:	543:	CATAGTTGCTGACTCCCGCTCGTGTAGATAAATCAGATACGGGCGGTACCATCTGG	5495
D:	449:	CATAGTTGCTGACTCCCGCTCGTGTAGATAAATCAGATACGGGCGGTACCATCTGG	4551
Q:	549:	CCCAGTGTGCAATGATACCGGAGACCCACGCTCACCGCTCCAGATTTATCAGCAAT	5555
D:	455:	CCCAGTGTGCAATGATACCGGAGACCCACGCTCACCGCTCCAGATTTATCAGCAAT	4611

QY	5556	AAACACGACCGCGGAGGCGGAGCGAGAGTGGTCTCTGCAACTTTTATCCGC	5615
DB	4612	AAACACGACCGCGGAGGCGGAGCGAGAGTGGTCTCTGCAACTTTTATCCGC	4671
QY	5616	CGAGTCTATTAATTGTTGCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTTAATAC	5675
DB	4672	CGAGTCTATTAATTGTTGCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTTAATAC	4731
QY	5676	CAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCAAGCTCGTCTGTTGGTAT	5735
DB	4732	CAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCAAGCTCGTCTGTTGGTAT	4791
QY	5736	ATTACAGTCCGGTTCCTCAACGATCAAGGGGAGTTACATGATCCCCCATGTTGTC	5795
DB	4792	ATTACAGTCCGGTTCCTCAACGATCAAGGGGAGTTACATGATCCCCCATGTTGTC	4851
QY	5796	AGCGGTTAGTCTCTCGGTCCTCCGATCGTGTGCAGAGTAAGTTGGCGCGAGT	5855
DB	4852	AGCGGTTAGTCTCTCGGTCCTCCGATCGTGTGCAGAGTAAGTTGGCGCGAGT	4911
QY	5856	ACTCATGTTATGCGCAGCACTGCATAATTCTCTTACTGTCAATGCCATCCGTAAAC	5915
DB	4912	ACTCATGTTATGCGCAGCACTGCATAATTCTCTTACTGTCAATGCCATCCGTAAAC	4971
QY	5916	TTCTGTGACTGTGAGTACTCAACCAAGTCAATTCAGAAATAGTGTATCGGCGC	5975
DB	4972	TTCTGTGACTGTGAGTACTCAACCAAGTCAATTCAGAAATAGTGTATCGGCGC	5031
QY	5976	TTGCTCTTCCCGGCGTCAATACGGGATAATACCGGCCACATAGCAGAACTTT	6035
DB	5032	TTGCTCTTCCCGGCGTCAATACGGGATAATACCGGCCACATAGCAGAACTTT	5091
QY	6036	GCTCATCATTTGGAAGAAAGTTCCTTCGGGGCGGAAAACTCTCAAGGATCTTACCGCT	6095
DB	5092	GCTCATCATTTGGAAGAAAGTTCCTTCGGGGCGGAAAACTCTCAAGGATCTTACCGCT	5151
QY	6096	ATCCAGTTCGATGTAAACCACTCGTGCACCCCACTGATCTTCAGCATCTTTTAC	6155
DB	5152	ATCCAGTTCGATGTAAACCACTCGTGCACCCCACTGATCTTCAGCATCTTTTAC	5211
QY	6156	CAGCGTTTCTGGGTGAGCAAAACAGGAAGGCAAAATGCGCAAAAAGGGAA	6215
DB	5212	CAGCGTTTCTGGGTGAGCAAAACAGGAAGGCAAAATGCGCAAAAAGGGAA	5271
QY	6216	GACACGGAATTTGAATACTCATACTCTTCTTTTCAATATTATTGAAGCAI	6275
DB	5272	GACACGGAATTTGAATACTCATACTCTTCTTTTCAATATTATTGAAGCAI	5331
QY	6276	GGGTATTGCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA	6335
DB	5332	GGGTATTGCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACA	5391
QY	6336	GGTTCGCGCACAATTTCCCGGAAAAAGTGCCACTGACGTC	6375
DB	5392	GGTTCGCGCACAATTTCCCGGAAAAAGTGCCACTGACGTC	5431

RESULT 8  
 AA289476  
 ID AA289476 standard; DNA; 5432 BP.  
 XX AA289476;  
 AC AA289476;  
 DT 22-JUN-2000 (first entry)  
 XX Transgenic APP DNA #2.  
 DE APP; amyloid precursor protein; gamma-secretase; neuroprotectiv  
 KW nootropic; transgenic; Alzheimer's disease; Down's syndrome; ds  
 XX Synthetic.  
 OS

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: 98DE-01056261.

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CHST MARION ROUSSEL DEUT GMBH.

58119/23.

f gamma-secretase by detection of A-beta peptide useful for gamma-secretase activity and for identifying inhibitors.

age 7-8: 16pp: German.

ion describes a novel method for the detection of human gamma y detection of a partial protein formed by cleavage of a ion encoded by a transgene containing a first nucleotide ich encodes a protein comprising the amino acid sequence (A) d nucleotide sequence which encodes a signal peptide. The the invention have neuroprotective and nootropic activity. is used to detect activity of gamma-secretase. The transgene ors are useful for the production of a transgenic cell or C. angenic C. elegans is useful in a method for the on of gamma-secretase activity. The transgenic C. elegans is in a method to identify inhibitors of the gamma-secretase he methods and transgenes are useful in research of disease. Inhibitors of gamma-secretase are useful in atment of Alzheimer's and possibly Down's syndrome. This codes a transgenic amyloid precursor protein (APP) which is n the method of the invention

32 BP; 1251 A; 1410 C; 1390 G; 1381 T; 0 U; 0 Other;

56.1%; Score 3578.4; DB 3; Length 5432;

ilarity 88.9%; Pred. No. 0;

Conservative 0; Mismatches 16; Indels 503; Gaps 5;

THE UNIVERSITY OF CHICAGO

GC TCCAGC TTTCTGAGGCGGAAGAACCACTGGGGCTCTAGGGGTATCCCCACGC 1809

1301

5'-TGTGCTGAGGCGGAAAGGAGCCAGCTGGGCTCTAGGGGATCTCCCAAGC-3'

CCTGTAGCGCGCATTAAGCGCGCGGTGTGGTTACGCGCAGCGTGACCGCTAC 1869

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84

TTTTCGCCGATTTTCGGCCTATTGGTTAAATAATGAGCTGATTTAACAAATTTAAACGC 2228

TTTTCGGGATTTTCGGCCTATTGGTTAAATAATGAGCTGATTTAACAAATTTAACGC 1721

[illegible]



NA3.

XX	Plasmid pCDNA3; pneumococcal surface protein A; PspA; infection
KW	Streptococcus pneumoniae; sepsis; otitis media; meningitis; bac
KW	pneumonia; vaccine; genetic immunisation; sa.
XX	
OS	Human herpesvirus 5.
OS	Chimeric.
XX	
PN	W09824927-A1.
PD	11-JUN-1998.
XX	
PF	04-DEC-1997; 97WO-US022847.
XX	
PR	04-DEC-1996; 96US-00759505.
XX	
PA	(UYAL-) UNIV ALABAMA.
XX	
PI	Briles DE, Medaniel LS, Curiel DT;
XX	
DR	WPI; 1998-333343/29.
XX	
PT	Plasmid containing pneumococcal epitope for expression in eukar
PT	cells - useful for eliciting immunological response to pneumoco
PT	infection or sepsis.
XX	
PS	Example 1; Fig 1B1 to 1B-5; 47pp; English.
XX	
CC	This is the DNA sequence of plasmid pCDNA3 (Invitrogen). A port
CC	gene (see AAV38298) that codes for respiratory syncytial virus
CC	glycoprotein G (RSVG) has been amplified, digested with KpnI an
CC	into KpnI-digested pCDNA3 upstream of the multiple cloning site
CC	and downstream of the human cytomegalovirus immediate early (HC
CC	promoter to create pGR41. A full-length coding sequence of Stre
CC	pneumoniae Rxi pneumococcal surface protein A (PspA) was then i
CC	into pGR41 to create a fusion between rsvg and PspA. Intramuscu
CC	immunisation of BALB/c mice with the resulting plasmid, designa
CC	pKSD2601, induced protection against an otherwise lethal challe
CC	capsular type 3 pneumococcus. A plasmid for expression of pneum
CC	epitope DNA in eukaryotic cells is claimed. The plasmid include
CC	promoter for driving expression in a eukaryotic cell (e.g. HCMV
CC	encoding a leader sequence (e.g. of RSVG) which facilitates exp
CC	translation through or transport of the expression product in a
CC	eukaryotic cell membrane, and DNA encoding a pneumococcal epit
CC	PspA. The invention also provides a vaccine comprising the plas
CC	suitable carrier or diluent, and optionally one or more cytokin
CC	encoding them, or a bacterial delivery system. The vaccine is u
CC	elicit an immunological response in a host, including humans, s
CC	to pneumococcal infection or sepsis. The plasmid can also be u
CC	express a pneumococcal epitope of interest in vitro. (Updated o
CC	2003 to standardise OS field)
XX	
SQ	Sequence 5446 BP; 1255 A; 1417 C; 1390 G; 1384 T; 0 U; 0 Other;
	Query Match 56.1%; Score 3578.4; DB 2; Length 5446;
	Best Local Similarity 88.9%; Pred. No. 0;
	Matches 4141; Conservative 0; Mismatches 16; Indels 503;
QY	1750 GAGCTCCAGCTTTCTTGAGCGGGAAGAACACAGCTGGGGCTCTAGGGGGTATCC
Db	1256 GGGCTCTATGGCTTCTTGAGCGGGAAGAACACAGCTGGGGCTCTAGGGGGTATCC
QY	1810 GCCTGTAGCGCGCATTTAAGCGCGCGGGTGTGTGTGTATACGCGCAGCGGTGAC
Db	1316 GCCTGTAGCGCGCATTTAAGCGCGCGGGTGTGTGTGTATACGCGCAGCGGTGAC
QY	1870 ACTTGCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTTCCTTCCTTCTTCGCG
Db	1376 ACTTGCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTTCCTTCTTCGCG
QY	1930 CGCGCGCTTTCCCGCTCAAGCTCTAAATCGGGGCG- TCCCTTTTGGGGTTCCGATTT
Db	1436 CGCGCGCTTTCCCGCTCAAGCTCTAAATCGGGGCGCATCGCTTTTGGGGTTCCGATTT



192 TTTACGGCACTCGACCCCAAAAACCTTGATTAGGTTGATGGTTCACTAGTGGCCATC 2048  
193 |||||  
194 TTTACGGCACTCGACCCCAAAAACCTTGATTAGGTTGATGGTTCACTAGTGGCCATC 1555  
195 |||||  
204 GCGCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCAGTCTCTTTAATAGTGACT 2108  
205 |||||  
206 GCGCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCAGTCTCTTTAATAGTGACT 1615  
207 |||||  
210 CTGTTTCCAAACTGGAAACAACACTCAACCCCTATCTCGGTCTATTTCTTTGATTATAAGG 2168  
211 |||||  
216 CTGTTTCCAAACTGGAAACAACACTCAACCCCTATCTCGGTCTATTTCTTTGATTATAAGG 1675  
217 |||||  
216 CATTTGCCGATTTTCGGCTATTGGTTTAAATAATGAGCTGATTTAACAAAAATTTAACGC 2228  
217 |||||  
217 CATTTTGGGGATTTTCGGCTATTGGTTTAAATAATGAGCTGATTTAACAAAAATTTAACGC 1735  
218 |||||  
222 GAATTAATCTGTGGAAATGCCCGGAGCTTGATATCCATTTTCGGATCTGATCAGCACT 2288  
223 |||||  
223 GAATTAATTT----- 1744  
224 |||||  
228 GAGGCGGAAGAAACACAGCTGTGGAAATGTGTGTCAGTTAGGTTGTGAAAGTCCCCAGGCT 2348  
229 |||||  
229 -----CTGTGGAATGTGTGTCAGTTAGGTTGTGAAAGTCCCCAGGCT 1787  
230 |||||  
234 CCCCCA-GCAGGCAAGATATGCAAGCATGTCATCTCAATTAGTCAGCAACAGGTTGGGA 2407  
235 |||||  
238 CCCCCAAGCAGCAGAGATATGCAAGCATGTCATCTCAATTAGTCAGCAACAGGTTGGGA 1847  
239 |||||  
240 AAGTCCCGCAGGCTCCCGCAGCAGCAGAGATATGCAAGCATGTCATCTCAATTAGTCAGCA 2467  
241 |||||  
241 AAGTCCCGCAGGCTCCCGCAGCAGCAGAGATATGCAAGCATGTCATCTCAATTAGTCAGCA 1907  
242 |||||  
246 AACCATAGTCCCGCCCTTAATCTCCGCCCATCCCGCCCTAACTCCGCCAGTTCGCCCCAT 2527  
247 |||||  
249 AACCATAGTCCCGCCCTTAATCTCCGCCCATCCCGCCCTAACTCCGCCAGTTCGCCCCAT 1967  
250 |||||  
252 TCTCCGCCCATCGCTGACTTAATTTTTTTTATTATGAGAGCCGAGGCGGCTCGGCC 2587  
253 |||||  
256 TCTCCGCCCATCGCTGACTTAATTTTTTTTATTATGAGAGCCGAGGCGGCTCGGCC 2027  
257 |||||  
258 TCTGAGCTATTCCAGAAATGATGAGGAGGCTTTTTTTGGAGGCTTAGGCTTTTCCAAAGAT 2647  
259 |||||  
261 TCTGAGCTATTCCAGAAATGATGAGGAGGCTTTTTTTGGAGGCTTAGGCTTTTCCAAAGAG 2087  
262 |||||  
264 C-----GATCAAGAGACAGGATGAGGATCGTTT 2675  
265 |||||  
268 CTTCCCGGAGCTTTGTATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGGATCGTTT 2147  
269 |||||  
269 CCGCATATTGAACAAGATGATGATGACGAGGTTCTCCGCCCGCTTTGGGTGGAGAGGCTA 2735  
270 |||||  
274 CCGTATTGAACAAGATGATGATGACGAGGTTCTCCGCCCGCTTTGGGTGGAGAGGCTA 2207  
275 |||||  
273 TCCGGCTATGACTGGGCACAAACAGACAAATCGGCTGCTCTGATCGCCCGCTTTCCGGCTG 2795  
274 |||||  
280 TCCGGCTATGACTGGGCACAAACAGACAAATCGGCTGCTCTGATCGCCCGCTTTCCGGCTG 2267  
281 |||||  
279 TTAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACTGTCGCGTCCCTGAAATGAA 2855  
280 |||||  
286 TTAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACTGTCGCGTCCCTGAAATGAA 2327  
287 |||||  
285 CTTGCAAGACGGGCGAGCGGCTATCGTGGCTGGCCACGACGCGGCTTCTTTCGCGAGCT 2915  
286 |||||  
292 CTTGCAAGACGGGCGAGCGGCTATCGTGGCTGGCCACGACGCGGCTTCTTTCGCGAGCT 2387  
293 |||||  
291 GTCTCTGAGCTTCACTGAAGCGGGAAGGAGCTGCTGCTGATTTGGCGAAGTCCCGGG 2975  
292 |||||  
298 GTCTCTGAGCTTCACTGAAGCGGGAAGGAGCTGCTGCTGATTTGGCGAAGTCCCGGG 2447  
299 |||||  
297 CAGGATCTCTGTGCTATCTCACTTGTCTTCCGCGAGAAAGTATCCATCATGCTGATGCA 3035  
300 |||||  
304 CAGGATCTCTGTGCTATCTCACTTGTCTTCCGCGAGAAAGTATCCATCATGCTGATGCA 2507

3036 ATCGCGCGCTGCTATACGCTTGTATCGGCTACCTGCCATTCGCCATTCGACCACCAAGC 3095  
3037 |||||  
2508 ATCGCGCGCTGCTATACGCTTGTATCGGCTACCTGCCATTCGCCATTCGACCACCAAGC 2567  
2509 |||||  
3096 CGCATCGAGGAGACAGTACTCGATGGAAGCGGCTTCTGTCGATCAGGATGA 3155  
3097 |||||  
2568 CGCATCGAGGAGACAGTACTCGATGGAAGCGGCTTCTGTCGATCAGGATGA 2627  
2569 |||||  
3156 GAAGAGCATCAGGCGCTCGCGCCAGCGCACTGTCGCCAGGCTCAAGGCGCG 3216  
3157 |||||  
2628 GAAGAGCATCAGGCGCTCGCGCCAGCGCACTGTCGCCAGGCTCAAGGCGCG 2687  
2629 |||||  
3216 GACGCGGAGGATCTCGTGTGACCCCATGCGCATGCGCTGTCGCCGATATCAT 3275  
3217 |||||  
2688 GACGCGGAGGATCTCGTGTGACCCCATGCGCATGCGCTGTCGCCGATATCAT 2747  
2689 |||||  
3276 AATGGCGGCTTTTCTGATTCATCGATGTGGCGGCTGGGTGTGGCGAACG 3325  
3277 |||||  
2748 AATGGCGGCTTTTCTGATTCATCGATGTGGCGGCTGGGTGTGGCGAACG 2807  
2749 |||||  
3336 GACATAGCGTTGGCTACCGTGATATTTGCTGAAGAGCTTGGCGCGCAATCGGCT 3395  
3337 |||||  
2808 GACATAGCGTTGGCTACCGTGATATTTGCTGAAGAGCTTGGCGCGCAATCGGCT 2867  
2809 |||||  
3396 TTCTCTGCTGCTTTACGGTATTCGCCGCTCCGATTCGACGCGCATCGCTTCTA 3455  
3397 |||||  
2868 TTCTCTGCTGCTTTACGGTATTCGCCGCTCCGATTCGACGCGCATCGCTTCTA 2927  
2869 |||||  
3456 CTTGACGAGTTCTTCTGAGCGGAGCTCTGGGTTTCAAAATGACCGACCAAGCG 3515  
3457 |||||  
2928 CTTGACGAGTTCTTCTGAGCGGAGCTCTGGGTTTCAAAATGACCGACCAAGCG 2987  
2929 |||||  
3516 ACCTGCCATCACAGAGATTTTCGATTCACCGCGCTTCTATGAAGGTTGGGCT 3575  
3517 |||||  
2988 ACCTGCCATC----- 2997  
3518 |||||  
3576 TCGTTTTCGGGAGCGCGCTGATGATCTTCAGCGCGGGATCTCATGCTGC 3625  
3577 |||||  
2998 ----- 2997  
3636 TCGCCACCTTAGGGGAGGCTAACTGAACACCGAAGGAGACAATACCGAAC 3685  
3637 |||||  
2998 ----- 2997  
3696 GCGCATGACGGCAATAAAAAGACAGAAATAAACGACGCTTGGGTGCTTGT 3755  
3697 |||||  
2998 ----- 2997  
3756 ACGGGGTTTCGGTCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCF 3815  
3757 |||||  
2998 ----- 2997  
3816 CCAATAGCGCCGGTTTCTTCTTTTCCCAACCCACCCCAAGTTCCGGTGA 3875  
3817 |||||  
2998 ----- 2997  
3876 AGGGCTCGAGCCAAACGTCGGGCGGCGAGGCTTGCCATAGCCTCAGTCTAC 3935  
3877 |||||  
2998 -----ACG 3006  
3936 CGATTCCACCGCGCTTCTATGAAGGTTGGGCTTCGGAATCGTTTTCGGGA 3995  
3937 |||||  
3007 CGATTCCACCGCGCTTCTATGAAGGTTGGGCTTCGGAATCGTTTTCGGGA 3066  
3008 |||||  
3996 CTTGGATGATCTCCAGCGCGGAGTCTCATGCTGAGTCTTCGCCGCCACCCAA 4054  
3997 |||||  
3067 CTTGGATGATCTCCAGCGCGGAGTCTCATGCTGAGTCTTCGCCGCCACCCAA 3126  
3068 |||||  
4056 TATTGAGCTTATAATGGTTTACAAATAAGCAATAGCATCACAAATTTACAAA 4115  
4057 |||||  
3127 TATTGAGCTTATAATGGTTTACAAATAAGCAATAGCATCACAAATTTACAAA 3184  
3128 |||||  
4116 ATTTTTCCTGCTATCTGATTTAGTTGTTGTTTCCAAACTCATCAATGATATCTTA 4175

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4267 AAAAGGATCTCAAGAGATCCTTTTGATCTTTTCTAOCGGGTCTGACGCTCAGTG  
5256 AAACCTCAGTTAAGGAGTTTTTGTGTCATGAGATTTATCAAAAAGGATCTTACCTTA  
4327 AAACCTCAGTTAAGGAGTTTTTGTGTCATGAGATTTATCAAAAAGGATCTTACCTTA  
5316 TTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTG  
4387 TTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTAAATTTG  
5376 CAGTTACCAATGCTTAATCAGTGAGGACCTTATCTCAGCGATCTGTCTATTG  
4447 CAGTTACCAATGCTTAATCAGTGAGGACCTTATCTCAGCGATCTGTCTATTG  
5436 CATAGTTGCTGACTCCCGCTGCTGTAGATACTACGATACGGAGGCTTACC  
4507 CATAGTTGCTGACTCCCGCTGCTGTAGATACTACGATACGGAGGCTTACC  
5496 CCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATC  
4567 CCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATC  
5556 AAACCAAGCCAGCCGAGGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGG  
4627 AAACCAAGCCAGCCGAGGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGAGCGG  
5616 CCAGTCTATTAAATTTGTTCCGGGAGCTAGAGTAAGTAGTTGCGCAGTTAATAG  
4687 CCAGTCTATTAAATTTGTTCCGGGAGCTAGAGTAAGTAGTTGCGCAGTTAATAG  
5676 CAAGTTGTTGCCATTCCTACAGGCATCGTGGTCTCACGCTCGTCTGTTGGTAT  
4747 CAAGTTGTTGCCATTCCTACAGGCATCGTGGTCTCACGCTCGTCTGTTGGTAT  
5736 ATTCAAGCTCGGTTTCCAAACGATCAAGCGAGTTACATGATCCCGCATGTTGTG  
4807 ATTCAAGCTCGGTTTCCAAACGATCAAGCGAGTTACATGATCCCGCATGTTGTG  
5796 AGCGTTAGCTCTTCCGTCCTCGATCGTTGTCAGAGTAAGTTGCGCGCAGT  
4867 AGCGTTAGCTCTTCCGTCCTCGATCGTTGTCAGAGTAAGTTGCGCGCAGT  
5856 ACTCATGTTATGCGCAGCATCTGATATTTCTTTACTGTGATGCCATCCGTAAG  
4927 ACTCATGTTATGCGCAGCATCTGATATTTCTTTACTGTGATGCCATCCGTAAG  
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5047 TTGCTCTTCCCGCGCTCAATACGGGATAATACCGCGCCATACAGCAGAACTTT  
6036 GCTCATCAATGCGAAAACGTTCTTCCGGGCGAAAACCTCTCAAGGATCTTACCGCT  
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5167 ATCCAGTTGAGTGTAAACCACTGCTGACCCCACTGATCTTTCAGCATCTTTTAC  
6156 CAGGTTTCTGGGTGAGCAAAAAACAGGAGGCAAAAAACGCGCAAAAAAGGGAAT  
5227 CAGGTTTCTGGGTGAGCAAAAAACAGGAGGCAAAAAACGCGCAAAAAAGGGAAT  
6216 GACACGGAAATGTTGAATACTCATCTCTCTTCTTTTCAATATTATTGAAGCAT  
5287 GACACGGAAATGTTGAATACTCATCTCTCTTCTTTTCAATATTATTGAAGCAT  
6276 GGGTTATGCTCATGAGGATACATATTGAAATGTAATTTAGAAAAATAACA  
5347 GGGTTATGCTCATGAGCGGATACATATTGAAATGTAATTTAGAAAAATAACA



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Db 2998 -----  
Qy 3816 CCAATACGCGCGGCTTTCTTCCTTTTCCCAACCCCAACCCCAAGTTTCGGGTGA  
Db 2998 -----  
Qy 3876 AGGCTCGACGACCAACGTCGGGGCGGAGGGCCCTGCCATAGCCTCAGTGTCTACG  
Db 2998 -----ACG  
Qy 3936 CGATTCCACCGCGCTTCTTATGAAAGGTTGGGCTTCGGAATCGTTTTCGGGA  
Db 3007 CGATTCCACCGCGCTTCTTATGAAAGGTTGGGCTTCGGAATCGTTTTCGGGA  
Qy 3996 CTGATGATCTTCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCAACCCCA  
Db 3067 CTGATGATCTTCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCAACCCCA  
Qy 4056 TATTGCAGCTTATATGTTTACAAATAAAGCAATAGCATCAAAATTTTCAAAA  
Db 3127 TATTGCAGCTTATATGTTTACAAATAAAGCAATAGCATCAAAATTTTCAAAA  
Qy 4116 ATTTTCTTCACTGCAATCTAGTTGTGTTTGTCCAAACTCATCAATGTATCTTA  
Db 3187 ATTTTCTTCACTGCAATCTAGTTGTGTTTGTCCAAACTCATCAATGTATCTTA  
Qy 4176 CTGATACCGTGCACCTCTAGCTAGAGCTTGGCGTATCATGTTCTATAGCTGTT  
Db 3247 CTGATACCGTGCACCTCTAGCTAGAGCTTGGCGTATCATGTTCTATAGCTGTT  
Qy 4236 GTGAAATGTTTATCGGCTCAAAATTCACACAAATACGAGCCGGAAGCATAAA  
Db 3307 GTGAAATGTTTATCGGCTCAAAATTCACACAAATACGAGCCGGAAGCATAAA  
Qy 4296 AGCTGGGCTGCTTAATGAGTGAAGTAACTCAATTAATTCGTTGGCTCACT  
Db 3367 AGCTGGGCTGCTTAATGAGTGAAGTAACTCAATTAATTCGTTGGCTCACT  
Qy 4356 TTTTCGCTGCGGGAACCTGTGCTGCCAGCTGCATTTAATGAAATCGGCAACCGGC  
Db 3427 TTTTCGCTGCGGGAACCTGTGCTGCCAGCTGCATTTAATGAAATCGGCAACCGGC  
Qy 4416 AGGCGGTTTGGCTATTTGGGCGCTCTTCGCTTTCCTCGCTCACTGACTCGCTGGC  
Db 3487 AGGCGGTTTGGCTATTTGGGCGCTCTTCGCTTTCCTCGCTCACTGACTCGCTGGC  
Qy 4476 CGTTTCGCTGCGGAGCGGTATCAGCTCACTCAAAAGCGGTATACGCTTATC  
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Qy 4536 ATCAGGGATAAACGAGGAAGAACATGTGAGCAAAAGCGGCAAAAGGCGCAG  
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Qy 4596 TAAAAAGCGCGGTTGCTGGCGTTTTCATAGGCTTCGCGCCCTTCGAGCA  
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Qy 4656 AAATCGAGCTCAAGTCAAGGTGGCGAAACCGGACAGGACTATTAAGATACCA  
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Qy 4716 TCCCTTCGGAAGCTCCCTCGTGGCGCTCTTCCTGTTCCGACCTTCGCGCTTACCGG  
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Qy 4776 GTCCGCTTTTCTTCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAACGCTGAG  
Db 3847 GTCCGCTTTTCTTCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAACGCTGAG  
Qy 4836 CAGTTTCGCTGAGTGTGCTTCGCTCCAGCTGGGCTGTGTCAGCAACCCCGCT  
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D 350 CAGTTCGGTGTAGTGTGCTTCCGCTCAAGCTGGGCTGTGTGCGACGAACCCCGGTTACGCC 3966  
Q 453 GAGCGCTGGCCCTTATPCGGTAACTATCGTCTTGAGTCCAAACCCCGGTAAAGACACGACTT 4955  
D 356 CAGCGCTGGCCCTTATPCGGTAACTATCGTCTTGAGTCCAAACCCCGGTAAAGACACGACTT 4026  
Q 455 ATGCGCACTGGCAGCAGCCACTGGTAAACAGATATAGCAGAGCGAGGTATGTAGCGGTGC 5015  
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D 414 CTGCGCTCTGCTGAAGCAGATTACCTTCGGAAGAGTGGTAGCTCTTTGATCCGGCAA 4206  
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D 420 ACAACCCACCGCTGTAGCGGTGGTTTTTTTGTGTTGCAACGACGAGATTAGCGCGAGAA 4266  
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Q 531 CTATAATTAATAATGAATTTAAATCAATCTAAAGTATATATAGTAAACTTGGTCTGA 5375  
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Q 537 CAGTTACCAATGCTTAATCAGTCAGGACCATCTCTCAGCGATCTGTCTATTCTGTTTCATC 5435  
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D 462 AACACGAGCAGCGGAGGCGGAGGCGGAGAGTGTCTTGCAACTTTATCCGCTCCAT 4686  
Q 561 CAGTCTATTAATTTGTCGGGAGGAGTGAAGTGTTCGCCAGTTAATAGTTTGG 5675  
D 468 CAGTCTATTAATTTGTCGGGAGGAGTGAAGTGTTCGCCAGTTAATAGTTTGG 4746  
Q 567 CACGTTGTTGCCATTGTACAGGCACTGTGGTGTACCGTCTGTGGTATGCTTC 5735  
D 474 CACGTTGTTGCCATTGTACAGGCACTGTGGTGTACCGTCTGTGGTATGCTTC 4806  
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D 480 ATTCAGTCTCGGTTCCCAACGATCAAGGCGGAGTTACATGATCCCCCATGTTGTGCAAAA 4866  
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D 498 TTCTGTGACTGTGTGAGTACTCAACCAAGTCAATCTGAGAAATAGTGTATGCGGACCGAG 5046

RESULT 11  
ABL53540

ID ABL53540 standard; DNA; 5446 BP.

XX ABL53540;

XX 10-JUN-2002 (first entry)

XX Vector pcDNA3.

DE Vector; pcDNA3; heat shock protein 60; Hsp60; autoimmune disease.

XX insulins dependent diabetes mellitus; IDDM; DNA immunisation; vector.

XX CpG; antidiabetic; immunotherapy; gene therapy; ds.

XX Cytomegalovirus.

OS Bos taurus.

OS Unidentified.

OS Chimeric.

XX WO200216549-A2.

XX 28-FEB-2002.

XX 23-AUG-2001; 2001WO-IL000790.

XX 25-AUG-2000; 2000US-0227853P.

XX (VEDA ) YEDA RES & DEV CO LTD.

XX Cohen IR, Quintana FJ;

XX WPI; 2002-227369/28.

XX Treating or preventing an ongoing autoimmune disease e.g. diab.

XX comprises vaccination with a DNA sequence comprising a CpG motif.

XX Example 1; Page 48-52; 53pp; English.

XX The present sequence is that of vector pcDNA3, a multipurpose c

XX expression vector containing the cytomegalovirus (CMV) immediat

XX promoter, a polylinker and the bovine growth hormone polyadenyl

XX site. The vector also expresses neomycin resistance in eukaryot

XX Human heat shock protein 60 (hsp60) full-length cDNA was cloned



the control of the CMV promoter, creating plasmid pHsp60. In order to explore the potential of a DNA-based therapy of insulin labates mellitus (IDDM), the effect of immunisation of NOD spontaneously develop IDDM, with pHsp60 was examined. The pcDNA3 plasmid was as effective at inhibiting the of diabetes as was the pHsp60 plasmid. Despite the absence of A3 induced specific effects on the autoimmunity to Hsp60 on the NOD diabetogenic process: down-regulation of T-cell on and the induction of IgG2b antibodies to Hsp60 and its cognate p277. A CpG oligonucleotide (see ABL53541), present in amplicillin resistance gene, reproduced the effects of pcDNA3 autoimmunity and on the NOD diabetes. The invention therefore method for the treatment or prevention of autoimmune diseases using a DNA vaccine which includes a CpG motif and which encode antigen associated with autoimmune diseases especially

46 BP; 1255 A; 1417 C; 1390 G; 1384 T; 0 U; 0 Other;  
56.1%; Score 3578.4; DB 6; Length 5446;  
ilarity 88.9%; Pred. No. 0;  
Conservative 0; Mismatches 16; Indels 503; Gaps 5;

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D: ----- 2997  
Q: GCGATGACGGCAATAAAAGACAGATAAAACGACGGTGTGGGTGTTTGTTCATAA 3755  
D: ----- 2997  
Q: ACGGGGTTTCGCTCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCAATTGGGG 3815  
D: ----- 2997  
Q: CAAATAGCCCGGTTTCTTCTTTTCCCAACCCACCCCAAGTTTCGGGTGAGGCC 3875  
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D: CAAATCCACCGCGCTTCTATGAAGTTGGGCTTCGGAATCGTTTTCGGGAGCGCGG 3066  
Q: CCGATGATCCTCCAGCGCGGATCTCATGCTGGAGTCTTCGCCACCCCACTTGT 4055  
D: CCGATGATCCTCCAGCGCGGATCTCATGCTGGAGTCTTCGCCACCCCACTTGT 3126  
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D: CTGTATACCGTCCAGCTTAGCTGGGTAAATCATGTCTATAGCTTTCCTGT 3306  
Q: GTGAATTTGTTATCCGCTCAAAATTCACACAATACGAGCCGGAAGCAATAAGTGTA 4295  
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D: CTTTCGCTGCGGAGCGGTATCAGTCACTCAAAAGCGGTAAATACGTTATCCACAGA 3606  
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QY 5736 ATTCAGCTCCGGTCCCAACGATCAAGCGAGGAGTTATGATATCCCGCATGTTGTG 5795



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TAGTTGCTGACTCCCGCTGGTGTAGATAACTACGATACGCGAGGGCTTACCTATCTGG 5495  
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TAGTTGCTGACTCCCGCTGGTGTAGATAACTACGATACGCGAGGGCTTACCTATCTGG 5202  
|||||  
CCAGTGTGCAATGATACCGGAGACCCAGCTCAGCGCTCCAGATTTATCAGCAAT 5555  
|||||

Db 5203 CCCAGTGTGCTCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATC  
Qy 5556 AACCAGCAGCCGAGGAGGCGGAGCGCAAGATGGTCTCTGCAACTTTATCCGC  
Db 5263 AACCAGCAGCCGAGGAGGCGGAGCGCAAGATGGTCTCTGCAACTTTATCCGC  
Qy 5616 CAGTCTTAAATTTGTTGCGGGAAGCTAGAGTAAAGTAGTTGCGCAGTTAATAG  
Db 5323 CAGTCTTAAATTTGTTGCGGGAAGCTAGAGTAAAGTAGTTGCGCAGTTAATAG  
Qy 5676 CAAGTGTGTCATCTGCTACAGGATCGTGGTGTCAAGCTCGTGGTGTGTTAT  
Db 5383 CAAGTGTGTCATCTGCTACAGGATCGTGGTGTCAAGCTCGTGGTGTGTTAT  
Qy 5736 ATTCAAGCTCGGTTCCCAAGCATCAAGCGAGTTTACATGATCCCCCATTTGTG  
Db 5443 ATTCAAGCTCGGTTCCCAAGCATCAAGCGAGTTTACATGATCCCCCATTTGTG  
Qy 5796 AGCGTTTAGCTCTCTCGTCTCCGATCGTTGTGTCAGAAAGTAAAGTTGGCCGAGT  
Db 5503 AGCGTTTAGCTCTCTCGTCTCCGATCGTTGTGTCAGAAAGTAAAGTTGGCCGAGT  
Qy 5856 ACTCATGTTTATGCGAGCACTGCAATAATTTCTTTACTGTGATGCGATCCGTAAG  
Db 5563 ACTCATGTTTATGCGAGCACTGCAATAATTTCTTTACTGTGATGCGATCCGTAAG  
Qy 5916 TTCTGTGACTGTGCTGAGTACTCAACCAAGTCACTCTGAGAAATAGTGTATGCGCG  
Db 5623 TTCTGTGACTGTGCTGAGTACTCAACCAAGTCACTCTGAGAAATAGTGTATGCGCG  
Qy 5976 TTGCTCTTGGCCGCGTCAATACCGGATTAATACCGGCCCATAGCAGAACTTTT  
Db 5683 TTGCTCTTGGCCGCGTCAATACCGGATTAATACCGGCCCATAGCAGAACTTTT  
Qy 6036 GCTCATCATTTGGAATAAGCTTCTCGGGCGGAAACTCTCAAGGATCTTTACGCT  
Db 5743 GCTCATCATTTGGAATAAGCTTCTCGGGCGGAAACTCTCTCAAGGATCTTTACGCT  
Qy 6096 ATCCAGTTTCGAGTAAACCACTCTGTCACCCAACTGATCTTTTTCAGCATCTTTTAC  
Db 5803 ATCCAGTTTCGAGTAAACCACTCTGTCACCCAACTGATCTTTTTCAGCATCTTTTAC  
Qy 6156 CAGCGTTTCTGGGTGAGCAAAACAGGAAGCAAAATGCCGCAAAAAAGGGAAT  
Db 5863 CAGCGTTTCTGGGTGAGCAAAACAGGAAGCAAAATGCCGCAAAAAAGGGAAT  
Qy 6216 GACACGGAATTTGGAATCTATCTCTCTCTTTTCAATATTTTGAAGCAT  
Db 5923 GACACGGAATTTGGAATCTATCTCTCTCTTTTCAATATTTTGAAGCAT  
Qy 6276 GGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACA  
Db 5983 GGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACA  
Qy 6336 GGTTCGCGCAATTTCCCGAAAGTCCACCTGACGTC 6375  
Db 6043 GGTTCGCGCAATTTCCCGAAAGTCCACCTGACGTC 6082

## RESULT 13

AAD56211

ID AAD56211 standard; DNA; 6082 BP.

XX AAD56211;

XX AAD56211;

DT 07-AUG-2003 (first entry)

XX Human AB-PG1-XG1-026 PSMA antibody light chain DNA.

DE Human; Prostate specific membrane antigen; carcinoma; sarcoma;  
KW PSMA; melanoma; therapy; N-acetylated alpha-linked acidic dipep  
KW folate hydrolase; dipeptidyl dipeptidase IV; gamma-glutamyl hyc  
KW NALADase; antibody; ds.





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ATTGAGTTAATGTTTACAAATAGCAATAGCATCAAAATTTTCAAAATAAGC 3822  
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Db 3883 CTGTATACCGTGGACCTTAGCTAGAGCTTGGCGTAAATCATGTGTATAGCTGTT  
QY 4236 GTGAAATGTTATCCGCTCAATTTCCACAACATACGAGCCGGAAGCATATA  
Db 3943 GTGAAATGTTATCCGCTCAATTTCCACAACATACGAGCCGGAAGCATATA  
QY 4296 AGCTGCGGCTGCTTAATGAGTGAAGTAACTCAATTAATTTGCGTTGCGCTCACT  
Db 4003 AGCTGCGGCTGCTTAATGAGTGAAGTAACTCAATTAATTTGCGTTGCGCTCACT  
QY 4356 TTTTCCAGTTCGGGAAACCTGTGCTGCCAGCTGATTAATGAATCGGCAACCGCGC  
Db 4063 TTTTCCAGTTCGGGAAACCTGTGCTGCCAGCTGATTAATGAATCGGCAACCGCGC  
QY 4416 AGGCGGTTTGGGTATTTGGGGCTCTTCCGCTTCTCGCTCACTCACTCGCTGCG  
Db 4123 AGGCGGTTTGGGTATTTGGGGCTCTTCCGCTTCTCGCTCACTCACTCGCTGCG  
QY 4476 CGTTCCGCTGCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGTTTATC  
Db 4183 CGTTCCGCTGCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAAATACGTTTATC  
QY 4536 ATCAGGGGATAAACGAGGAAAGAAATGTTGAGCAAAAAGCCAGCAAAAGGCCAG  
Db 4243 ATCAGGGGATAAACGAGGAAAGAAATGTTGAGCAAAAAGCCAGCAAAAGGCCAG  
QY 4596 TAAAAAGCGCGGTTGCTGGCGTTTTCATAGGCTCGCCCTCGACGAGCA  
Db 4303 TAAAAAGCGCGGTTGCTGGCGTTTTCATAGGCTCGCCCTCGACGAGCA  
QY 4656 AAATCGAGCTCAAGTCAAGGTGCGGAAACCCGACAGGACTATAAGATACCA  
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Db 4963 AAACCTCAGGTTAAGGATTTTGGTCACTGAGATTAATAAAAGGATCTTCAACCTT



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D: 502 TTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATATAGTAAACCTTGGTCTGA 5082
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D: 508 CAGTTACCAATGCTTAATCAGTCAGGCACCTATCTCAGCGATCTGTCTATTCTGTTTCATC 5142
Q: 543 CATAGTTGCTGCTACTCCCGTCTGTGTAGATAAATACGATACGGGAGGGCTTACCATCTGG 5495
D: 514 CATAGTTGCTGCTACTCCCGTCTGTGTAGATAAATACGATACGGGAGGGCTTACCATCTGG 5202
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D: 520 CCCCAGTCTGCATGATGATCCGGAGAGCCACGCTCCACGGCTCCAGATTTATCAGCAAT 5262
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Q: 561 CAGTCTATTAATTTGTTGCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGGC 5675
D: 532 CAGTCTATTAATTTGTTGCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGGC 5382
Q: 567 CACGTTGTTGCCATTTGCTACAGGCATCGTGTGTACGCTGTGTTGGTAGTGGCTTC 5735
D: 538 CACGTTGTTGCCATTTGCTACAGGCATCGTGTGTACGCTGTGTTGGTAGTGGCTTC 5442
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D: 544 ATTACGCTCCGGTTCCCAACGATCAAGGCGAGTTTACATGATCCCCCAATGTTGCAAAA 5502
Q: 579 AGCGTTAGTCTCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTGGCCGACGTGTTATC 5855
D: 550 AGCGTTAGTCTCTTCGGTCTCCGATCGTTGTGAGAAGTAAGTGGCCGACGTGTTATC 5562
Q: 585 ACTCAGTTATGCGAGCATGATTAATCTTCTACTGTGATGCCATCGTAAGATGCTT 5915
D: 556 ACTCAGTTATGCGAGCATGATTAATCTTCTACTGTGATGCCATCGTAAGATGCTT 5622
Q: 591 TCTGTGACTGTGTGAGTACTCAACCAAGTCAATCTGAGATAGTGTATGCGGACCGAG 5975
D: 562 TCTGTGACTGTGTGAGTACTCAACCAAGTCAATCTGAGATAGTGTATGCGGACCGAG 5682
Q: 597 TGGCTTTGCGCGGCTCAATACGGGATAATACCGGCCACATAGCAGAACTTTAAAGT 6035
D: 568 TGGCTTTGCGCGGCTCAATACGGGATAATACCGGCCACATAGCAGAACTTTAAAGT 5742
Q: 599 GATCATCTTGGAAACGTTCTTCGGGGCGAAGTCTCAGGATCTTACCCTGTTGAG 6095
D: 570 GATCATCTTGGAAACGTTCTTCGGGGCGAAGTCTCAGGATCTTACCCTGTTGAG 5802
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D: 580 ATCCAGTTTCGATGTAACCCACTGTCACCCCAACTGATCTTACGATCTTTTACTTTTAC 5862
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D: 592 GATCAGGAAATGTTGAATCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5982
Q: 599 GGTATTGTTCTCATGAGGGATACATATTTGAATGTTATTGAAAAATAAACAATAGG 6335
D: 598 GGTATTGTTCTCATGAGGGATACATATTTGAATGTTATTGAAAAATAAACAATAGG 6042
Q: 599 GGTTCGCGGCAATTTTCCCGGAAAGTGCCACCTGACGTC 6375
D: 594 GGTTCGCGGCAATTTTCCCGGAAAGTGCCACCTGACGTC 6082
```

## RESULT 14

AAD56210  
ID AAD56210 standard; DNA; 6082 BP.

XX AAD56210;

XX AC (first entry)

XX DT 07-AUG-2003 (first entry)

XX DE Human AB-PGI-XGI-006 PSMA antibody light chain DNA.

XX KW Human; Prostate specific membrane antigen; carcinoma; sarcoma; PSMA; melanoma; therapy; N-acetylated alpha-linked dipeptide hydrolase; dipeptidyl dipeptidase IV; gamma-glutamyl hydrolase; NAALADase; antibody; ds.

OS Homo sapiens.

XX WO2003034903-A2.

XX PD 01-MAY-2003.

XX PF 23-OCT-2002; 2002WO-US033944.

XX PR 23-OCT-2001; 2001US-0335215P.

XX PR 07-MAR-2002; 2002US-0362747P.

XX PR 20-SEP-2002; 2002US-0412618P.

PA (PSMA-) PSMA DEV CO LLC.

XX Maddon FJ, Donovan GP, Olson WC, Schuelke N, Gardner J, Me

WPI; 2003-403281/38.

PT Novel isolated antibody which binds to epitope on prostate spec

PS Claim 1; Page 206-209; 238pp; English.

CC The invention relates to an antibody or its antigen-binding fra

XX Sequence 6082 BP; 1421 A; 1595 C; 1546 G; 1520 T; 0 U; 0 Other;

Query Match 56.1%; Score 3578.4; DB 7; Length 6082;

Best Local Similarity 88.9%; Pred. No. 0;

Matches 4141; Conservative 0; Mismatches 16; Indels 503; 5;

QY 1750 GAGCTCCAGCTTTTCTGAGCGGAAAGAACACGAGCTGGGGCTTAGGGGTATCC

DB 1892 GGGCTCTATGCTTCTGAGCGGAAAGAACACGAGCTGGGGCTTAGGGGTATCC

QY 1810 GCCCTGTAGCGCGCATTAAGCGCGGGTGTGTGGTTAGCGCGCGTGCAC

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|||||TTGCCAGCGCCCTAGCGCCCGCTCCCTTTCCGCTTTCTCCCTTTCTCCCTTTCTCGCCACGGTT 2071  
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|||||TACGCACTCTGACCCCAAACTTTGATAGGGTGTGATGCTTCACTAGTGGGCCATC 2191  
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|||||CCTGATAGCGGTTTTTCGCCCTTTGACGTTGGAGTCCAGCTTTCTTTAATAGTGGACT 2251  
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|||||TTTTCGGGATTTTCGGGCTATTGGTTAAAAAATGAGCTGATTTAAACAAAAATTTAACGC 2371  
|||||ATTAATTTGTGGAAATGCGCGGAGCTTGTATATATCCATTTTCGGATCTCATCAGCACT 2288  
|||||ATTAATTTGTGGAAATGCGCGGAGCTTGTATATATCCATTTTCGGATCTCATCAGCACT 2380  
|||||GGCGGAAGAAACCAAGCTGTGGATGTGTCTCAGTTAGGGTGTGGAAGTCCCGAGCT 2348  
|||||-----CTGTGGAAATGTGTCTCAGTTAGGGTGTGGAAGTCCCGAGCT 2423  
|||||CCA-GCAGGCAGAAATGCAAGCATGCTCAATTAAGTCAAGCAACAGGTGTGGA 2407  
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|||||TCCGCCCATGCGTGAATTTTATTTATGAGAGGCGAGGCGCCCTCGGCC 2663  
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Db 2964 CTCGAGGACGAGGCGAGCGGCTATCTGTGGCTGGCCACGAGCGGGGCTTCTTTCG  
Qy 2916 GTGCTCGAGCTTGTCTCACTGAAGCGGGGAAGGGACTGGCTGTCTATTGGCGGGAAGTG  
Db 3024 GTGCTCGAGCTTGTCTCACTGAAGCGGGGAAGGGACTGGCTGTCTATTGGCGGGAAGTG  
Qy 2976 CAGGATCTCTGTCTCATCTCACTTGTCTTGTCTCGGAGAAAGTATCCATCATGGCT  
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Qy 3036 ATGCGGCGGCTGCTACGCTTGTATCCGGCTACCTGCCCATTTGCAACCAAGCG  
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Qy 3096 CGCATCGAGCGAGCACGCTACTCGGATCGAAGCGGCTTGTGATCAGGATGAT  
Db 3204 CGCATCGAGCGAGCACGCTACTCGGATCGAAGCGGCTTGTGATCAGGATGAT  
Qy 3156 GAGAGCATCAGGGGCTCGGCGCAGCCGAACTGTTCCGCAAGGCTCAAGGGCGAGC  
Db 3264 GAGAGCATCAGGGGCTCGGCGCAGCCGAACTGTTCCGCAAGGCTCAAGGGCGAGC  
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Db 3564 CTTGACAGGTTCTTCTGAGCGGAGCTCTGGGGTTCGAAATGACCGACCGAGCGA  
Qy 3516 ACCTGCGCATCAGGATTTGATTTCCACCGCGGCTTCTATGAAAGGTTGGGCT  
Db 3624 ACCTGCGCATC-----  
Qy 3576 TCGTTTTCCGGGACGCGCGCTGGATGATCTCTCCAGCGCGGGGATCTCATGTGG  
Db 3634 -----  
Qy 3636 TCGCCCACTAGGGGGAGGCTAACTGAAACACGAGAGGAGACAATACCGGAAG  
Db 3634 -----  
Qy 3696 GCGCATGACGCAATAAAGACAGAAATAAAGCAOAGTGTGGGTCTTGT  
Db 3634 -----  
Qy 3756 ACGCGGGGTTCCGTTCCAGGGCTGGCACTCTGTGATACCCCAACGAGACCCCA  
Db 3634 -----  
Qy 3816 CCAATACGCGCGGTTTTCTTCTTTTCCCAACCCCAACCCCAAGTTCCGGGTGA  
Db 3634 -----  
Qy 3876 AGGGCTCGACCAACGTTCCGGGCGGCGAGGCGCTGCGCATAGCTCAGTGTCTACG  
Db 3634 -----ACG  
Qy 3936 CGATTTCCACCGCGCTTCTATGAAAGGTTTCGGGCTTTCGAAATCGTTTTTCGGG  
Db 3643 CGATTTCCACCGCGCTTCTATGAAAGGTTTCGGGCTTTCGAAATCGTTTTTCGGG

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D: CTGTATACCGTCAACCTCTAGCTAGAGCTTGGGTAATCATGTGTCATAGCTTTCCTGT 3942  
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D: GTCAAAATTTGTATCCGCTCAAAATCCACACATACGAGCCGGAGCATAAAGTGTA 4002  
Q: AGCTGGGGTCCCTAATGAGTGAGCTAACTCACATTAATTTGGCTCACTGCCCGC 4355  
D: AGCTGGGGTCCCTAATGAGTGAGCTAACTCACATTAATTTGGCTCACTGCCCGC 4062  
Q: TTTCAGTCCGGAAACCTGTGTCGAGCTAGCTGCAATTAATGAATCGGCCAAGCGCGGGAG 4415  
D: TTTCAGTCCGGAAACCTGTGTCGAGCTAGCTGCAATTAATGAATCGGCCAAGCGCGGGAG 4122  
Q: AGCGGTTTTCGTAATTTGGGGCTCTTCGGCTTCTCGCTCACTGATCTCGCTGCGCTCGGT 4475  
D: AGCGGTTTTCGTAATTTGGGGCTCTTCGGCTTCTCGCTCACTGATCTCGCTGCGCTCGGT 4182  
Q: GGTTCGCTGCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGA 4535  
D: GGTTCGCTGCGCGAGCGGTATCAGCTCACTCAAAAGCGGTAATACGGTTATCCACAGA 4242  
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D: ATCAGGGGTAACGCGAGGAAGAACATGTAGCAAAAGGCCAGAAAGGCCAGGAACCG 4302  
Q: TAAAAAGCGCGCTGCTGCGGTTTTCATAGGCTCCGCCCGCTGACGAGCATCACAA 4655  
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Q: AATCGACGCTCAAGTCAGAGTGCGGAAACCCGACAGGACTATAAGATACCGCGGT 4715  
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D: GTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGAGGTATCT 4542  
Q: CATTCGCTGAGTTCGTTTCGCTCCAAAGCTGGGCTGTGTGCAAGAACCCCGCTTCAGCC 4895  
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D: CACCGCTGGCCCTTATCCGTTAATCTATGCTTTGAGTCCAAAGCTGAGTAAAGTAT 4662  
Q: ATCCGCACTGGCAGCAGCTGTAACAGGATTTAGCAGGAGGATAGTAGGGCGGTGC 5015  
D: ATCCGCACTGGCAGCAGCTGTAACAGGATTTAGCAGGAGGATAGTAGGGCGGTGC 4722  
Q: TACAGAGTTCTTGAAGTGGTGGCTTAACCTAGCGGCTACCTAGAGGAACAGTATTTGGTAT 5075  
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Q: CTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGAT 5076  
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Q: AAAAAACACCGCTGTAGCGGTGGTTTTTTTGTTCGAAGCAGCAGATTACGC 5136  
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D: TTTAAATTAATAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTC 5023  
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Q: CATAGTTGCCTGACTCCCGTCTGTAGATACTACGATACGGAGGGCTTAC 5436  
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D: CCCAGTGTGCATGATACCGCGAGACCCACGCTCACGGCTCCAGATTAT 5203  
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D: CAGTCTATTAATTTGTTCGGGAAGCTAGAGTAAGTTCGCCAGTTAATAC 5323  
Q: CAACGTTGTGCTATGCTACAGGCATCTGTGGTGTCAAGTTCGCTGTTGGT 5676  
D: CAACGTTGTGCTATGCTACAGGCATCTGTGGTGTCAAGTTCGCTGTTGGT 5383  
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D: TTGCTCTTCCCGCGGTCAATAACGGGTAATACCGGCCACATAGCAGAACTTT 5743  
Q: GCTCATCTTGAAAAACGTTCTTCGGGGGAAAACTCTCAAGGATCTTACCGCT 6096  
D: GCTCATCTTGAAAAACGTTCTTCGGGGGAAAACTCTCAAGGATCTTACCGCT 5743  
Q: ATCCAGTTTCGATGTAACCCACTCGTGCAACCACTGATCTTCAGGATCTTTTAC 5803  
D: ATCCAGTTTCGATGTAACCCACTCGTGCAACCACTGATCTTCAGGATCTTTTAC 6156  
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D: CAGCGTTTCTGGGTGAGCAAAAAAGGAGGCAAAATGCCGAAAAAAGGGAAT 6216

[illegible]

andard; DNA: 6085 BP.

(first entry)

1-XG1-069 PSMA antibody light chain DNA.

tate specific membrane antigen; carcinoma; sarcoma; cancer; oma; therapy; N-acetylated alpha-linked acidic dipeptidase; olase; dipeptidyl dipeptidase IV; gamma-glutamyl hydrolase; antibody; ds.

၈

3-A2.

• ; 2002WO-US033944.

; 2001US-0335215P.  
; 2002US-0362747P.  
; 2002US-0412618P.

A DEV CO LLC.

Donovan GP, Olson WC, Schuelke N, Gardner J, Ma D;

03281/38.

ted antibody which binds to epitope on prostate specific antigen, and competitively inhibits binding of second antibody et epitope on the antigen, useful for treating prostate

ge 216-219; 238pp; English.

[illegible]

CC polypeptide, gamma-glutamyl hydrolase activity of a gamma-gluta  
CC hydrolase polypeptide. The present sequence is human PSMA antib  
CC chain DNA

XX SQ	Sequence 6085 BP; 1412 A; 1601 C; 1556 G; 1516 T; 0 U; 0 Other;
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Best Local Similarity	88.9%; Pred. No. 0;
Matches 4141; Conservative	0; Mismatches 16; Indels 503;

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Db 1895 GGGCTCTATGGCTTCTGAGGCCGGAAGAACCAAGCTGGGGCTCTAGGGGGTATCC

Qy 1810 GCCTGTAGCGCGCATTTAAGCGCGGGTGTGGTGTATACGCGCAGCGTGAC  
Db 1955 GCCTGTAGCGCGCATTTAAGCGCGGGTGTGGTGTATACGCGCAGCGTGAC

Qy	1870	ACTTGCCAGCGCCCTAGCGCCGCTCCTTTGCTTTCTTCCCTTCTCTTCTCGC
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Qy	1930	CGCGGGCTTTCCCGGTCAGCTCTAAATCGGGGC-TCCCTTTAGGGTTCCGATT
	2075	CGCGGGCTTTCCCGGTCAGCTCTAAATCGGGGCATCCCTTTAGGGTTCCGATT
Db		

Qy 1989 TTTACGGCACCTCGACCCCAAAAACCTTGATTAGGGTGATGGTTACGTTAGTGG  
2135 TTTACGGCACCTCGACCCCAAAAACCTTGATTAGGGTGATGGTTACGTTAGTGG

**Qy**      2049    GCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAAATAG  
             |||||  
**D6**      2195    GCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAAATAG

Qy	2109	CTTGTTC	CAAACT	GGAA	CAAC	ACTCA	ACCC	TATCT	CGG	CTAT	CTTTT	GATT
Db <th>2255</th> <th>CTTGTTC</th> <th>CAAACT</th> <th>GGAA</th> <th>CAAC</th> <th>ACTCA</th> <th>ACCC</th> <th>TATCT</th> <th>CGG</th> <th>CTAT</th> <th>CTTTT</th> <th>GATT</th>	2255	CTTGTTC	CAAACT	GGAA	CAAC	ACTCA	ACCC	TATCT	CGG	CTAT	CTTTT	GATT

Qy 2169 GATTTTGGCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTAAACAAAATT  
|||  
2315 GATTTTGGGGAATTTCGGCCTATTGGTTAAAAAATGAGCTGATTAAACAAAATT

Qy	2229	GAATTAATTCTGTGGAATGCCCGGAGCTTGTAATCCATTTCGGATCTGATC
Db	2375	GAATTAATT-----

Qy 2289 GAGCGGAAAGAACACGCTGTGGAAATGTGTGTCACTTAGGTAGGTGGAAAGTCCC  
Db 2384 -----CTGTGGAAATGTGTGTCACTTAGGTAGGTGGAAAGTCCC

Qy	2349	CCCCA-GCAGG	CAGGAAGTATG	CAAGCATG	CAATCT	CAATTAGT	CAGCAAC	CCAGG
Db	2427	CCCCAGG	CAGGAGTATG <th>CAAGCATG</th> <th>CAATCT</th> <th>CAATTAGT</th> <th>CAGCAAC</th> <th>CCAGG</th>	CAAGCATG	CAATCT	CAATTAGT	CAGCAAC	CCAGG

<b>Qy</b>	2408	AAGTCCCCAGGCTCCCGCAGGCAGAGTATGCCAAGCATGCATCTCAATTAG 
<b>Dd</b>	2487	AAGTCCCCAGGCTCCCGCAGGCAGAGTATGCCAAGCATGCATCTCAATTAG 

Qy		2468
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Qy	2528	TCTCGCCCCATGGCTGACTAA	TTTTTTTATTATGTCAGAGGCCGCGCC
Db	2607	TCTCGCCCCATGGCTGACTAA	TTTTTTTATTATGTCAGAGGCCGCGCC

Qy	2588	TCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCTAGGCTTTTTC
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Qy	2648	C	-----GATCAAGAGACAGGATGAGG
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08:16:05 2004

**ug-10-668-496-2.mq**

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6036	GCTCATCATTTGGAAAAAGCTTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGGCT	Qy
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6096	ATCCAGTTTCGATGTAAACCCCACTCGTGACACCAACTGATCTTCAAGCATCTTTTAC	Qy
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6216	GACACGGAAATGTTGAATATCTCATCTCTTCTCTTTTCAATATATTTGAAGCAT	Qy
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6336	GGTTCCCGCGCACATTTTCCCCGAAAAAGTGCCACTGACGTC	Qy
6046	GGTTCCCGCGCACATTTTCCCCGAAAAAGTGCCACTGACGTC	Db

Search completed: July 15, 2004, 08:09:01  
Job time : 2340 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

C - nucleic search, using sw model

July 14, 2004, 03:02:49 ; Search time 387 Seconds  
(without alignments)  
9141.633 Million cell updates/sec

US-10-668-496-2  
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IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

682709 seqs, 277475446 residues

Number of hits satisfying chosen parameters: 1365418

Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Issued Patents NA:\*

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5: /cgn2\_6/ptodata/2/ina/PCTUS COMB.seq.\*

6: /cgn2\_6/ptodata/2/ina/backfiles1.seq.\*

is the number of results predicted by chance to have a  
re greater than or equal to the score of the result being printed,  
is derived by analysis of the total score distribution.

# SUMMARIES

Seq	Query	Match	Length	DB	ID	Description
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578	1	56.1	6238	3	US-08-646-538-5	Sequence 5, Appli
578	1	56.1	6238	3	US-09-503-222-5	Sequence 5, Appli
578	1	56.1	6338	4	US-09-646-691B-4	Sequence 4, Appli
578	1	56.1	8578	4	US-09-796-575-3	Sequence 3, Appli
578	1	56.1	10443	4	US-09-845-917A-25	Sequence 25, Appli
578	1	56.1	16656	1	US-08-741-881-1	Sequence 1, Appli
578	1	56.1	16656	1	US-08-739-158-1	Sequence 1, Appli
578	1	56.1	16656	3	US-08-739-167-1	Sequence 1, Appli
578	1	56.1	16656	3	US-08-404-796-1	Sequence 1, Appli
578	1	56.1	16656	3	US-08-931-869-1	Sequence 1, Appli
578	1	56.1	16656	4	US-09-350-399-1	Sequence 1, Appli
578	1	56.1	16656	4	US-09-236-140A-1	Sequence 1, Appli
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557	3	55.8	6802	4	US-08-809-513A-6	Sequence 3, Appli
536	1	55.5	6896	2	US-08-627-151A-6	Sequence 6, Appli
533	1	55.4	7573	4	US-09-837-863-27	Sequence 27, Appli
478	1	54.6	6253	2	US-08-627-151A-5	Sequence 5, Appli
455	1	54.2	7106	1	US-08-188-281B-8	Sequence 8, Appli
455	1	54.2	7106	1	US-08-453-552-5	Sequence 5, Appli
455	1	54.2	7106	2	US-08-710-637-5	Sequence 5, Appli
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## ALIGNMENTS

RESULT 1

US-08-235-277-1

; Sequence 1, Application US/08235277

; Patent No. 5733543

; GENERAL INFORMATION:

; APPLICANT: NABEL, GARY J

; APPLICANT: WOFFENDIN, CLIVE

; APPLICANT: YANG, NIN-SUN

; APPLICANT: SHEEHY, MICHAEL J

; TITLE OF INVENTION: INTRODUCTION OF HIV-PROTECTIVE GENES

; TITLE OF INVENTION: INTO CELLS BY PARTICLE-MEDIATED GENE TRANSFER

; NUMBER OF SEQUENCES: 1

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

; ADDRESSEE: P.C.

; STREET: 1755 S. Jefferson Davis Highway, Suite 400

; CITY: Arlington

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/235,277

; FILING DATE: 29-APR-1994

; CLASSIFICATION: 436

; ATTORNEY/AGENT INFORMATION:

; NAME: Oblon, No. 5733543man F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 6042-008-68

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 413-3000

; TELEFAX: (703) 413-2220

; TELEX: 248855 OPAT UR

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5653 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: Other nucleic acid

US-08-235-277-1

Query Match 56.2%; Score 3580.2; DB 1; Length 5653;  
Best Local Similarity 88.6%; Pred. No. 0;  
Matches 4158; Conservative 0; Mismatches 63; Indels 470;

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|||||

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|||||

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publication US/08646538  
 7881

# MATION:

Pavliakis, George N.  
 Gaitanaris, George A.  
 Stauber, Roland H.  
 Vournakis, John N.

VENTION: Mutant Aequorea victoria Fluorescent  
 VENTION: Proteins Having Increased Cellular Fluorescence

SEQUENCES: 37

NCE ADDRESS:

: Townsend and Townsend and Crew LLP  
 Two Embarcadero Center, 8th Floor

n Francisco

alifornia

USA

11-3834

ADABLE FORM:

PE: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

Patent in Release #1.0, Version #1.30

LICATION DATA:

ON NUMBER: US/08/646,538

TE: No. 6027881 yet assigned

ACTION: 435

ENT INFORMATION:

ber, Kenneth A.

ION NUMBER: 31,677

/DOCKET NUMBER: 015280-249000

CATION INFORMATION:

: (415) 576-0200

(415) 576-0300

OR SEQ ID NO: 5:

ABACTERISTICS:

6238 base pairs

cleic acid

IESS: single

linear

PE: DNA

1..6238

ORMATION: /note= "pFRED7"

Query Match 56.1%; Score 3578.4; DB 3; Length 6238;  
 Best Local Similarity 88.9%; Pred. No. 0;  
 Matches 414; Conservative 0; Mismatches 16; Indels 503;

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	5899	GCTCATTCATTTGGAAAAACGTTCTTCCGGGGCGGAAGAACTCTCAAGGAATCTTTTACCGETC	
DB			
	6096	ATCCAGTTTCGCATTGAACCACTCGTGCGAACCAAACGTGATCTTTTCAGCATCTTTTATTC	
QY			
	5959	ATCCAGTTTCGCATTGAACCACTCGTGCGAACCAAACGTGATCTTTTCAGCATCTTTTATTC	
DB			
	6156	CAGCGTTTTCTCGGTGAGCAAAAACAAGGAAGGCCAAAATGCCGCAAAAAAAAAAGGGAAT	
QY			
	6019	CAGCGTTTTCTCGGTGAGCAAAAACAAGGAAGGCCAAAATGCCGCAAAAAAAAAAGGGAAT	
DB			
	6216	GACACGGAAATCTTGAATACTCATACTCTTCTCTTTTCCAATATTATTTCAGAGCAT	
QY			
	6079	GACACGGAAATCTTGAATACTCATACTCTTCTCTTTTCCAATATTATTTCAGAGCAT	
DB			
	6276	GGGTATTTCCTCATGAGCGGATACATATTTCGAATGTATTTAGAAAAAATAAACA	
QY			
	6139	GGGTATTTCCTCATGAGCGGATACATATTTCGAATGTATTTAGAAAAAATAAACA	
DB			
	6336	GGTTCCGGCACATTTCCCAGAAAAGAATGCCACCTGACGTC 6375	
QY			
	6199	GGTTCCGGCACATTTCCCAGAAAAGAATGCCACCTGACGTC 6238	
DB			
	<b>RESULT 3</b>		
	US-09-503-222-5		
	; Sequence 5, Application US/09503222		
	; Patent No. 6265548		
	; GENERAL INFORMATION:		
	; APPLICANT: Pavlakis, George N.		
	; APPLICANT: Gaitanaris, George A.		
	; APPLICANT: Stauber, Roland H.		
	; APPLICANT: Vournakis, John N.		
	; TITLE OF INVENTION: Mutant Aquorea victoria Fluorescent		
	; TITLE OF INVENTION: Proteins Having Increased Cellular Fluores		
	; NUMBER OF SEQUENCES: 37		
	; CORRESPONDENCE ADDRESS:		
	; ADDRESSEE: Townsend and Townsend and Crew LLP		
	; STREET: Two Embarcadero Center, 8th Floor		
	; CITY: San Francisco		
	; STATE: California		
	; COUNTRY: USA		
	; ZIP: 94111-3834		
	; COMPUTER READABLE FORM:		
	; MEDIUM TYPE: Floppy disk		
	; COMPUTER: IBM PC compatible		
	; OPERATING SYSTEM: PC-DOS/MS-DOS		
	; SOFTWARE: Patent In Release #1.0, Version #1.30		
	; CURRENT APPLICATION DATA:		
	; APPLICATION NUMBER: US/09/503,222		
	; FILING DATE:		
	; CLASSIFICATION:		
	; PRIOR APPLICATION DATA:		
	; APPLICATION NUMBER: US/08/646,538		
	; FILING DATE:		
	; ATTORNEY/AGENT INFORMATION:		
	; NAME: Weber, Kenneth A.		
	; REGISTRATION NUMBER: 31,677		
	; REFERENCE/DOCKET NUMBER: 015280-249000		
	; TELECOMMUNICATION INFORMATION:		
	; TELEPHONE: [415] 576-0200		
	; TELEFAX: [415] 576-0300		
	; INFORMATION FOR SEQ ID NO: 5:		
	; SEQUENCE CHARACTERISTICS:		
	; LENGTH: 6238 base pairs		
	; TYPE: nucleic acid		
	; STRANDEDNESS: single		
	; TOPOLOGY: linear		
	; MOLECULE TYPE: DNA		
	; FEATURE:		
	; NAME/KEY: -		
	; LOCATION: 1..6238		



HER INFORMATION: /note= "pPRED7"		
Q1	175	GAGTCCAGCTTTCTCAGGGGAGAAACAGCTGGGGCTTAGGGGTATCCCCACGC 1809
B1	204	CGGCTCTATGGCTTCTCAGGGGAGAAACAGCTGGGGCTTAGGGGTATCCCCACGC 2107
M1	41	Conservative 0; Mismatches 16; Indels 503; Gaps 5;
Q1	181	GCCTGTAGCGGCGCATTAAGCGCGCGGGTGCTGTACGCGCAGCGGTACCGGTAC 1869
B1	210	GCCTGTAGCGGCGCATTAAGCGCGCGGGTGCTGTACGCGCAGCGGTACCGGTAC 2167
Q1	187	ACTTGCCAGCGCCTAGCGCCCGCTCTCTTTGCTTTCTTCCCTTCTCTCGCCACGTT 1929
B1	216	ACTTGCCAGCGCCTAGCGCCCGCTCTCTTTGCTTTCTTCCCTTCTCTCGCCACGTT 2227
Q1	193	CGCGGCTTTCCCGTCAAGCTCTAAATCGGGC-TCGCTTTAGGGTTCGGATTAGTGC 1988
B1	222	CGCGGCTTTCCCGTCAAGCTCTAAATCGGGC-TCGCTTTAGGGTTCGGATTAGTGC 2287
Q1	198	TTTACGGCACCTCGACCCCAAAACCTTGATTAGGGTGATGGTTTACGTAGTGGCCATC 2048
B1	228	TTTACGGCACCTCGACCCCAAAACCTTGATTAGGGTGATGGTTTACGTAGTGGCCATC 2347
Q1	204	GCCTGTAGACGGTTTTTCCGCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGACT 2108
B1	234	GCCTGTAGACGGTTTTTCCGCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGACT 2407
Q1	210	CTTGTTCCAACTGGACACACTCAACCTATCTCGGCTCTATCTTTGATTATAAGG 2168
B1	240	CTTGTTCCAACTGGACACACTCAACCTATCTCGGCTCTATCTTTGATTATAAGG 2467
Q1	216	GATTTTGGCGATTTCGGCTTAITGGTTTAAATAAGTGCATTTTACAAAATTTAACGC 2228
B1	246	GATTTTGGCGATTTCGGCTTAITGGTTTAAATAAGTGCATTTTACAAAATTTAACGC 2527
Q1	222	GAATTAATTCGTGGAAATGCCGGAGCTTTGTATATCAATTTTCGGATCTGATCAGCACT 2288
B1	252	GAATTAATTCGTGGAAATGCCGGAGCTTTGTATATCAATTTTCGGATCTGATCAGCACT 2536
Q1	228	GAGGCGGAAAGAACAGCTGTGGAAATGTGTGTAGTTAGGTGTGAAAGTCCCGAGGCT 2348
B1	253	CTGTGAAATGTGTGTAGTTAGGTGTGAAAGTCCCGAGGCT 2579
Q1	234	CCCCA-GCAGGCGAAGATGCAAAAGCATGATCTCAATTAGTCAGCAACAGGTGTGGA 2407
B1	258	CCCCAGGCGAAGATGCAAAAGCATGATCTCAATTAGTCAGCAACAGGTGTGGA 2639
Q1	240	AAGTCCCGAGGCTCCCGCAGGAGAGATGCAAAAGCATGATCTCAATTAGTCAGCA 2467
B1	264	AAGTCCCGAGGCTCCCGCAGGAGAGATGCAAAAGCATGATCTCAATTAGTCAGCA 2699
Q1	246	ACCATAGTCCCGCCCTTAATCTCGCCCATCCCGCCCTTAATCTCGCCCATTCGCGCCAT 2527
B1	270	ACCATAGTCCCGCCCTTAATCTCGCCCATCCCGCCCTTAATCTCGCCCATTCGCGCCAT 2759
Q1	252	TCTCCGCCCATGGCTGACTTAATTTTATTTATGTCAGAGGCGCGGCGCTCGGCC 2587
B1	276	TCTCCGCCCATGGCTGACTTAATTTTATTTATGTCAGAGGCGCGGCGCTCTGCC 2819
Q1	258	TCTGAGCTATTCCAGAAAGTGTAGGAGGCTTTTGGAGGCTTAGGCTTTTGCAGAGAT 2647
B1	282	TCTGAGCTATTCCAGAAAGTGTAGGAGGCTTTTGGAGGCTTAGGCTTTTGCAGAGAT 2879
Q1	264	C-----GATCAAGACAGCATGAGATCGTTT 2675
B1	288	CTCCCGGAGCTTGTATATCCATTTTCGGATCTGATCAAGACAGCATGAGATCGTTT 2939
Q1	267	CGCATGATTGAACAAGATGGAATGACAGAGGTTCTCCGGCGCTTGGGTGGAGAGGCTA 2735
B1	379	CGCATGATTGAACAAGATGGAATGACAGAGGTTCTCCGGCGCTTGGGTGGAGAGGCTA 3789
Q1	2736	TTCCGCTTATGACTGGGCACACAGACAATCGGCTGCTCTGATGCGCGCGTGT 2795
B1	3000	TTCCGCTTATGACTGGGCACACAGACAATCGGCTGCTCTGATGCGCGCGTGT 3059
Q1	2796	TCAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGCTGCCCT 2835
B1	3060	TCAGCGCAGGGGCGCCCGGTTCTTTTGTCAAGACCGACCTGTCCGCTGCCCT 3119
Q1	2856	CTGCAAGACGAGGAGCGCGGCTATCGTGGCTGGCCACGACGCGGCTTCTCTTG 2915
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B1	3180	GTGCTCGACCTTGTCTGCTGAAGCGGGAAGGAGCTGGCTGTATTTGGCGGAAGT 3239
Q1	2976	CAGGATCTCTGTCTCATCTCACTTGTCTCTGCGGAGAAAGTATCCATCATGGC 3035
B1	3240	CAGGATCTCTGTCTCATCTCACTTGTCTCTGCGGAGAAAGTATCCATCATGGC 3299
Q1	3036	ATGCGGGGCTGATACGCTTGTATCGGCTTACCTGCCCATTCGACCAACCAAGC 3095
B1	3300	ATGCGGGGCTGATACGCTTGTATCGGCTTACCTGCCCATTCGACCAACCAAGC 3359
Q1	3096	CGCATCGAGGAGCACCTACTCGGATGGAAGCGGCTCTTGTGATCAGATGAT 3155
B1	3360	CGCATCGAGGAGCACCTACTCGGATGGAAGCGGCTCTTGTGATCAGATGAT 3419
Q1	3156	GAAGAGATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGAG 3215
B1	3420	GAAGAGATCAGGGGCTCGCGCCAGCCGAACTGTTGCCAGGCTCAAGGCGAG 3479
Q1	3216	GACGCGAGGATCTCTGTGTGACCCATGGGATGCTGTTGCCGGAATATCAT 3275
B1	3480	GACGCGAGGATCTCTGTGTGACCCATGGGATGCTGTTGCCGGAATATCAT 3539
Q1	3276	AATGGCGGCTTTCTCGATTTCATCGACTGTGGCGGCTGGGTGGCGGAGCG 3335
B1	3540	AATGGCGGCTTTCTCGATTTCATCGACTGTGGCGGCTGGGTGGCGGAGCG 3599
Q1	3336	GACATAGCTTGCTACCGGTGATATTGCTGAAGAGCTTTGGCGGCAATGGGCT 3395
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B1	3660	TTCTCTGCTTTTACGGTATCGCGCTCCGATTCGAGGCGATCGGCTTCTAT 3719
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Q1	3756	ACGCGGGGTTCCGTCAGGGGCTGCACTCTCTGCTGATATCCCAACCGAGACCCCA 3815
B1	3790	ACGCGGGGTTCCGTCAGGGGCTGCACTCTCTGCTGATATCCCAACCGAGACCCCA 3789

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D	589	GCTCATCATTTGGAAAAAGCTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAG	5958
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D	607	GACACGGAAATGTTGAAATATCATACTCTCTCTTTTTCATATATTATTGGAAGCATTTATCA	6138
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C	633	GGTTCGCGGCACATTTCCCGGAAAAGTGCCACCTGACGTC	6375
D	619	GGTTCGCGGCACATTTCCCGGAAAAGTGCCACCTGACGTC	6238

0.3e  
0.3a

-69.3-4  
e 4 Application US/09646691B

**AL INFORMATION:**

APPLICANT: McCONNELL, Stephen, J. and SPINELLA, Dominic, G.  
TITLE OF INVENTION: PEPTIDE LIGANDS FOR THE ERYTHROPOIETIN RECEPTOR

NUMBER OF SEQUENCES: 90

**CORRESPONDENCE ADDRESS:**

ADDRESSEE: Gen-Probe Incorporated  
STREET: 10210 Genetic Center Drive

**CITY: San Diego**

STATE: CA

**COUNTRY: USA**

ZIP: 92121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

**OPERATING SYSTEM: DOS**

SOFTWARE: FASTSEQ FOR WINDOWS VERSION 1.0  
 CPU: 486 APPLICATION DATE: 11/11/94

APPLICATION DATA: 11/08/1945 5019

REFUGATION NUMBER: US/09/646,691B  
FILING DATE: 20-Sep-2000

CLASSIFICATION: ~~Unknown~~

CLASSIFICATION: UNCLASSIFIED  
PRICE APPLICATION DATA:

APPLICATION NUMBER: &lt;Unknown&gt;

FILING DATE: <Unknown>

**ATTORNEY/AGENT INFORMATION:**

**NAMB: Gritzmacher, Christine A**

REGISTRATION NUMBER: 40,627

REFERENCE/DOCKET NUMBER: CB9701-A01

**TEL. COMMUNICATION INFORMATION:**

**TELEPHONE: 619-410-8926**

TELEFAX: 619-410-8928

TELEX: <Unknown>

FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 6338 base pairs

Query Match	56.1%	Score 3578.4	DB 4	Length 6338
Best Local Similarity	88.9%	Pred. No. 0		
Matches 4141	Conservative	0	Mismatches 16	Indels 503
QY	1750	GAGCTCCAGCTTTTCTGAGCGGGAAAGAAACAGCTGGGGCTCTAGGGGGTATC		1809
DB	2148	GGGCTCTATGGCTTCTGAGCGGAAAGAAACAGCTGGGGCTCTAGGGGGTATC		2277
QY	1810	GCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGGTGTTTACGGCGACGGTGAA		1869
DB	2208	GCCCTGTAGCGCGCATTAAGCGCGCGGGTGTGGTGTTTACGGCGACGGTGAA		2267
QY	1870	ACTTGCAGCGCCCTAGCGGCCGCTCTTTTGGCTTTCTCCCTTCCTTTCTCG		1929
DB	2268	ACTTGCAGCGCCCTAGCGGCCGCTCTTTTGGCTTTCTCCCTTCCTTTCTCG		2307
QY	1930	CGCGGGCTTTCCCGCTCAAGCTCTAAATCGGGC		1988
DB	2328	CGCGGGCTTTCCCGCTCAAGCTCTAAATCGGGC		2386
QY	1989	TTTACGGCACCTCGACGCCAAAAAATTGATTAGGGTGATGGTTCAGTAGTGC		2048
DB	2388	TTTACGGCACCTCGACGCCAAAAAATTGATTAGGGTGATGGTTCAGTAGTGC		2447
QY	2049	GCCCTGATAGACGGTTTTTCCGCTTTTGAAGTTGGAGTCCACGTTCTTTAATA		2108
DB	2448	GCCCTGATAGACGGTTTTTCCGCTTTTGAAGTTGGAGTCCACGTTCTTTAATA		2507
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DB	2508	CTTGTTCCAACTGGAACAACACTCAACCTATCTCGGTCTATCTTTTGATT		2567
QY	2169	GATTTTCCGATTTCCGCTTATGGTTTAAAAAATGAGCTGATTTAACAAAAAT		2228
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QY	2229	GAATTAATCTGTGGAAATGCCGGAGCTGTGTATATCCATTTTCGATCTGATC		2288
DB	2628	GAATTAATCTGTGGAAATGCCGGAGCTGTGTATATCCATTTTCGATCTGATC		2686
QY	2289	GAGCGGAAAGAACACGCTGTGGAATGTGTGTGTCAGTTAGGGTGTGGAAGTCC		2348
DB	2637	-----CTGTGGAATGTGTGTGTCAGTTAGGGTGTGGAAGTCC-----		2699
QY	2349	CCCCA- GCAGGCAGAGATATGCAAGCATGCATCTCAATTAGTCAGCAACCAG		2407
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QY	2408	AAGTCCCGAGGCTCCCGCAGCAGAGATATGCAAGCATGCATCTCAATTAG		2467
DB	2740	AAGTCCCGAGGCTCCCGCAGCAGAGATATGCAAGCATGCATCTCAATTAG		2799
QY	2468	ACCATAGTCCCGCCCTTAATCTCGGCCATCCCGCCCTTAATCTCGGCCAGTTCC		2527
DB	2800	ACCATAGTCCCGCCCTTAATCTCGGCCATCCCGCCCTTAATCTCGGCCAGTTCC		2859
QY	2528	TCTCCGCCCCCATGGCTGACTAATTTTTTTTTTATTATGACAGAGCCGAGCCGCC		2587
DB	2860	TCTCCGCCCCCATGGCTGACTAATTTTTTTTTTATTATGACAGAGCCGAGCCGCC		2919
QY	2588	CTTGAGCTATTCAGAAGTAGTGAGAGGCTTTTTTGGAGGCTTAGGCTTTTTC		2647
DB	2920	CTTGAGCTATTCAGAAGTAGTGAGAGGCTTTTTTGGAGGCTTAGGCTTTTTC		2979
QY	2648	C-----GATCAAGACACAGGATGAGGA		2676
DB	2980	CTCCCGGAGCTTGTATATCCATTTTTCGATCTGATCAAGACAGGATGAGGA		3039
QY	2676	CGCATGATTGAACAAGATGATTGACGACGAGTTCTTCGGCCGCTTTGGGTGAG		2734
DB	3040	CGCATGATTGAACAAGATGATTGACGACGAGTTCTTCGGCCGCTTTGGGTGAG		3099
QY	2736	TTCCGCTATCACTGGGCACAAACAGACAATCCGCTGTCTGTATGCCGCGCGTGTTC		2793



Q:	495:	A	TCCGCACTGCGCAGCGCCACTGTGTAAACAGGATTTAGCAGCGGAGGTATGTAGCGGTGC	5015
D:	491	A	TCCGCACTGCGCAGCGCCACTGTGTAAACAGGATTTAGCAGCGGAGGTATGTAGCGGTGC	4978
Q:	501:	T	CAGAGGTTCTTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAAGAAACAGTATTGTGTAT	5075
D:	497	T	CAGAGGTTCTTTGAAGTGGTGGCCCTAACTACGGCTACACTAGAAGGACAGTATTGTGTAT	5038
Q:	507:	CT	CGGCTCTGCTGAAGCCAGTTACTCTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA	5135
D:	503	CT	CGGCTCTGCTGAAGCCAGTTACTCTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA	5098
Q:	513:	A	CAAAACACCGCTGCTAGCGTGGTTTTTTTGTGTTGCAAGCAGCAGATTAACGCGCAGAA	5195
D:	509	A	CAAAACACCGCTGCTAGCGTGGTTTTTTTGTGTTGCAAGCAGCAGATTAACGCGCAGAA	5158
Q:	513:	A	AAAGGATCTCAAGAAGATCCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGA	5255
D:	515	A	AAAGGATCTCAAGAAGATCCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGA	5218
Q:	525:	A	AACTCAGGTTAAAGGATTTTGGTCATGAGATTAACAAAAGGATCTTCACTAGATCCCT	5315
D:	521	A	AACTCAGGTTAAAGGATTTTGGTCATGAGATTAACAAAAGGATCTTCACTAGATCCCT	5278
Q:	531:	T	TAAATTTAAAAATGAAGTTTAAATCAATCTAAAGTATATACAGTAAGTAACTTGGTCTGA	5375
D:	527	T	TAAATTTAAAAATGAAGTTTAAATCAATCTAAAGTATATACAGTAAGTAACTTGGTCTGA	5338
Q:	537:	C	AGTTACCAATGCTTAATCAAGTAGGCAACCTATCTCAGCGATCTGTCTATTTTCGTTCACTC	5435
D:	533	C	AGTTACCAATGCTTAATCAAGTAGGCAACCTATCTCAGCGATCTGTCTATTTTCGTTCACTC	5398
Q:	543:	C	ATAGTTGCGCTGATCCCGGTCGTTAGATAAATCAATACAGTAGGAGGCGTTACCATCTGG	5495
D:	539	C	ATAGTTGCGCTGATCCCGGTCGTTAGATAAATCAATACAGTAGGAGGCGTTACCATCTGG	5458
Q:	549:	C	CCAGTGTCTGCAATGATACCGCAGACCCACCGCTCACCGGCTCCAGATTTATCAGCAAT	5555
D:	545	C	CCAGTGTCTGCAATGATACCGCAGACCCACCGCTCACCGGCTCCAGATTTATCAGCAAT	5518
Q:	555:	A	ACACGCGCAGCGGAAGGGCCGAGCGCAGAAGTGGTCTTGCAACTTTATCCGCTCCAT	5615
D:	551	A	ACACGCGCAGCGGAAGGGCCGAGCGCAGAAGTGGTCTTGCAACTTTATCCGCTCCAT	5578
Q:	561:	C	AGTCTATTAAATTTGTTCCGGGAGAGCTAGTAAGTAGTTCCGCAAGTAAATAGTTTGGC	5675
D:	557:	C	AGTCTATTAAATTTGTTCCGGGAGAGCTAGTAAGTAGTTTCCGCAAGTAAATAGTTTGGC	5638
Q:	567:	C	AAAGTTTGTGCCATTTGCTACAGGCATCTGTGGTGTACGCTCGTGTGTTGGTATGGCTTC	5735
D:	563:	C	AAAGTTTGTGCCATTTGCTACAGGCATCTGTGGTGTACGCTCGTGTGTTGGTATGGCTTC	5698
Q:	573:	A	TTACAGTCTCGGTTTCCCAACGATCAAGGCGAGTTACATGATCCGCCATGTTGTGCAAAA	5795
D:	569:	A	TTACAGTCTCGGTTTCCCAACGATCAAGGCGAGTTACATGATCCGCCATGTTGTGCAAAA	5758
Q:	579:	A	GGGTTAGTCTCTTCCGCTCCTCGATCGTTGTGTCAGAAAGTAAGTTGGCCCGCAGTTATC	5855
D:	575:	A	GGGTTAGTCTCTTCCGCTCCTCGATCGTTGTGTCAGAAAGTAAGTTGGCCCGCAGTTATC	5818
Q:	585:	A	CTCATGTGTTATGCGCAGCATGCAATAATCTCTTACTGTCTATGTCATCCGTAAGATGCTTT	5915
D:	581	A	CTCATGTGTTATGCGCAGCATGCAATAATCTCTTACTGTCTATGTCATCCGTAAGATGCTTT	5878
Q:	591:	T	CTGTGACTGGTGAGTACTCAACCAAGTCAATCTCTAGAAATAGTGTATGCGGCGACCGAG	5975
D:	587:	T	CTGTGACTGGTGAGTACTCAACCAAGTCAATCTCTAGAAATAGTGTATGCGGCGACCGAG	5938
Q:	597:	T	GTCTTGTCCCGCGGCTCAATAACGGGATATAACCGCGCCACATAGCAGAACTTTTAAAGT	6035
D:	593:	T	GTCTTGTCCCGCGGCTCAATAACGGGATATAACCGCGCCACATAGCAGAACTTTTAAAGT	5998

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RESULT 5
US-09-796-575-3
; Sequence 3, Application US/09796575
; Patent No. 6632671
; GENERAL INFORMATION:
; APPLICANT: Geneseques, Inc.
; TITLE OF INVENTION: NANOCAPSULE ENCAPSULATION SYSTEM AND METHOD
; FILE REFERENCE: G32.12-0001
; CURRENT APPLICATION NUMBER: US/09/796,575
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/185,282
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 8578
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Supplied by Invitrogen of Carlsbad, California
US-09-796-575-3

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Query Match	56.1%	Score 3578.4	DB 4	Length 8578	
Best Local Similarity	88.9%	Pred. No. 0			
Matches 4141	Conservative 0	Mismatches 16	Indels 503		
Qy	1750	GAGTCAGCTTTTCTAGCGCGAAGAACACAGCTGGGCTCTAGGGGGTATCC		1409	1409
Db	4388	GGGCTCTATGGCTTCTGAGCGGAAAGAACACAGCTGGGCTCTAGGGGGTATCC		1410	4447
Qy	1810	GCCTGTAGCGGGCGCATTAAGCGCGCGGTGTGGTTACGGCGACAGCTGAC		1869	1869
Db	4448	GCCTGTAGCGGGCGCATTAAGCGCGCGGTGTGGTTACGGCGACAGCTGAC		1870	4507
Qy	1870	ACTTGGCAGCGCCTAGCGCCCGCTCTTTCGCTTTCTCCCTTCCTTTCTCGC		1929	1929
Db	4508	ACTTGGCAGCGCCTAGCGCCCGCTCTTTCGCTTTCTCCCTTCCTTTCTCGC		1930	4567
Qy	1930	CGCCGGCTTTCCCGCTCAAGCTCTAAATCGGGC-TCCCTTTAGGGTCCGATT		1988	1988
Db	4568	CGCCGGCTTTCCCGCTCAAGCTCTAAATCGGGCATCCCTTTAGGGTCCGATT		1989	4627
Qy	1989	TTTACGCGCACTCGACCCCAAAAACTTGATTAGGGTGATGGTTACAGTAGTGG		2048	2048
Db	4628	TTTACGCGCACTCGACCCCAAAAACTTGATTAGGGTGATGGTTACAGTAGTGG		2049	4687
Qy	2049	GCCTGATAGCGGTTTTTCGCCCTTTTGACGTTGGAGTCCACGCTCTTTTAATAG		2108	2108



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QY 3156 GAAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTCCGCCAGGCTCAAGGCGAGC  
Db 5760 GAAGAGCATCAGGGGCTCGCGCAGCCGAACTGTTCCGCCAGGCTCAAGGCGCGC  
QY 3216 GACGGCAGAGATCTCGTCTGAGACCCATGCGGATCGCTTTCGCCGAATATCATG  
Db 5820 GACGGCAGAGATCTCGTCTGAGACCCATGCGGATCGCTTTCGCCGAATATCATG  
QY 3276 AATGGCGCTTTTCTGATTCATGCACTGTGGCGCGGCTTGGGTGGGCGACCGC  
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QY 3336 GACATAGCTTGGCTACCGGTGATTTGCTGAAGAGCTTGGCGCGGAATGGGCT  
Db 5940 GACATAGCTTGGCTACCGGTGATTTGCTGAAGAGCTTGGCGCGGAATGGGCT  
QY 3396 TTCCTCTGCTTTTACCGGTATCGCGCTCCCGATTCGAGGCGCATCGGCTTCTAT  
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QY 3456 CTTGACGAGTTCTTCTGAGCGGAGCTCTGGGTTTCGAAATGACCGACCAAGCGA  
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QY 3516 ACCTGCCATCAGAGATTTTCGATTCACCGCGGCTTCTATGAAGGTTGGGCT  
Db 6120 ACCTGCCATC-----  
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Db 6130 -----  
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Db 6130 -----ACG  
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QY 3996 CTGGATGATCTCCAGCGGGGATCTCATGCTGGGTTCTTCGCCACCCCA  
Db 6199 CTGGATGATCTCCAGCGGGGATCTCATGCTGGGTTCTTCGCCACCCCA  
QY 4056 TATTGACGCTTAAATGGTTAAATAAAGCAATAGCATCAAAATTTTCAAAA  
Db 6259 TATTGACGCTTAAATGGTTAAATAAAGCAATAGCATCAAAATTTTCAAAA  
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Db 6319 ATTTTTTTCATGCACTTCTAGTGTGGTTTTCGAACTCATCAATGATCTTA  
QY 4176 CTGTATACCGTCGACCTCTAGCTAGAGCTTCGCGTAATCATGTGCTATAGCTGT  
Db 6379 CTGTATACCGTCGACCTCTAGCTAGAGCTTCGCGTAATCATGTGCTATAGCTGT



Q2	423	G	T	G	A	A	T	T	G	T	A	T	C	G	C	T	C	A	A	T	T	C	A	C	A	A	C	A	T	A	T	C	G	A	C	G	A	G	A	C	A	T	A	A	G	T	G	T	A	A		4299																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
D6	643	G	T	G	A	A	T	T	G	T	A	T	C	G	C	T	C	A	A	T	T	C	A	C	A	A	C	A	A	C	A	T	A	T	C	G	A	C	G	A	G	A	C	A	T	A	A	G	T	G	T	A	A		6498																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																	
Q7	429	A	G	C	T	G	G	G	T	G	C	T	A	A	T	G	A	G	T	A	A	C	T	C	A	C	A	T	T	A	A	T	T	T	G	C	G	T	C	A	T	G	C	T	C	A	T	G	C	C	G	C		4355																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
D6	649	A	G	C	T	G	G	G	T	G	C	T	A	A	T	G	A	G	T	A	A	C	T	C	A	C	A	T	T	A	A	T	T	T	G	C	G	T	C	A	T	G	C	T	C	A	T	G	C	C	G	C		6558																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																		
Q7	435	T	T	C	C	A	G	T	C	G	G	A	A	C	T	G	T	C	C	A	G	C	T	G	C	A	T	T	A	A	T	T	A	A	T	G	A	A	T	T	G	A	A	T	T	G	A	A		4415																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
D6	655	T	T	C	C	A	G	T	C	G	G	A	A	C	T	G	T	C	C	A	G	C	T	G	C	A	T	T	A	A	T	T	A	A	T	G	A	A	T	T	G	A	A	T	T	G	A	A		6618																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																						
Q7	441	A	G	C	G	G	T	T	G	G	T	A	T	T	G	G	C	C	T	T	C	G	G	T	C	T	C	T	C	G	C	T	C	A	T	G	C	T	G	C	T	G	C	T	G	C	T	G	C		4475																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
D6	661	A	G	C	G	G	T	T	G	G	T	A	T	T	G	G	C	C	T	T	C	G	G	T	C	T	C	T	C	G	C	T	C	A	T	G	C	T	G	C	T	G	C	T	G	C	T	G	C		6678																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																					
Q7	147	C	G	T	T	C	G	C	T	G	C	G	A	C	G	G	T	A	C	A	G	T	C	A	C	T	C	A	A	A	G	C	G	T	A	A	T	A	T	A	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T	T

5880	Db	 AAGTCCCAGGCTCCCCACAGCGCAGAGTAATGCAAGCATGCACTCAATTA
2468	QY	 ACCATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTAACTCCCGCCCAAGTTCC
5940	Db	 ACCATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTAACTCCCGCCCAAGTTCC
2528	QY	 TCTCGGCCCATGGCTGACATAATTTTTTTTATATATGACAGAGCCGAGGCGCGCC
6000	Db	 TCTCGGCCCATGGCTGACATAATTTTTTTTATATATGACAGAGCCGAGGCGCGCC
2588	QY	 TCTGAGCTATTCCAGAAAGTAGAGGAGGCTTTTTTGGAGGCTAGGCTTTTGC
6060	Db	 TCTGAGCTATTCCAGAAAGTAGAGGAGGCTTTTTTGGAGGCTAGGCTTTTGC
2648	QY	C----- GATCAAGAGACAGGATGAGGA
6120	Db	 CTCCCGGAGCTTGTAATCCATTTTCGGATCTGATCAAGAGACAGGATGAGGA
2676	QY	 CGCATGATTGAACAGAGTCGATTGCACGCAAGTTCTCCGGCCGCTTGGGTGGAG
6180	Db	 CGCATGATTGAACAGAGTCGATTGCACGCAAGTTCTCCGGCCGCTTGGGTGGAG
2736	QY	 TTCGGCTATGACTGGGCAACAAGACAATTCGGCTGCTCTGATGCCCCGCTGTTTC
6240	Db	 TTCGGCTATGACTGGGCAACAAGACAATTCGGCTGCTCTGATGCCCCGCTGTTTC
2796	QY	 TCAGCGAGGGGCGCCGGTTCTTTTGTCAAGACGACCTGTCCGGTGCCTCG
6300	Db	 TCAGCGAGGGGCGCCGGTTCTTTTGTCAAGACGACCTGTCCGGTGCCTCG
2856	QY	 CTGCAAGACAGGCGAGCGCGCTATCGTGGCTGGCCACGACGGGGCTTCCTTGC
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3036	QY	 ATGCGCGCGCTGCATACGCTTGATCCGGCTACTCTGCCACTTCGACCAACAAGCG
6540	Db	 ATGCGCGCGCTGCATACGCTTGATCCGGCTACTCTGCCACTTCGACCAACAAGCG
3096	QY	 CGCATCGAGCGAGCAGTACTCGATGGAAGCGGTCGTTGTCATCAGATGAT
6600	Db	 CGCATCGAGCGAGCAGTACTCGATGGAAGCGGTCGTTGTCATCAGATGAT
3156	QY	 GAAGAGCATCAGGGGCTCGCGCCAGCGAACTGTTGCGCAGGCTCAAGGCGAGC
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6720	Db	 GAAGCGAGGATCTCGTGTGTGACCCATGCGGATGCTCTGTCGGAATATCATG
3276	QY	 AATGGCCGCTTTTCTGATTTCACTGCTGCGCGGCTCGGTTGGCGGACCGC
6780	Db	 AATGGCCGCTTTTCTGATTTCACTGCTGCGCGGCTCGGTTGGCGGACCGC
3336	QY	 GACATAGCGTTGCTATCCCGTGATATTGCTGAAGAGCTTGGCGGGAATGGGCT
6840	Db	 GACATAGCGTTGCTATCCCGTGATATTGCTGAAGAGCTTGGCGGGAATGGGCT
3396	QY	 TTCTCTGCTTTTACGATATCGCGCTTCGGAATGCGAGCATCGCCTTCTAT
6900	Db	 TTCTCTGCTTTTACGATATCGCGCTTCGGAATGCGAGCATCGCCTTCTAT
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 TTCCGGCGCAATTTCCCGGAAAGTGCCACCTGACGTC 9478

plication US/08741881  
 9245

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Dubensky Jr, Thomas W  
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 Ibanez, Carlos E.  
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 Driver, David A.  
 Belli, Barbara A.

VENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS

SEQUENCES: 128

NCE ADDRESS:

: SEED and BERRY LLP  
 6300 Columbia Center, 701 Fifth Avenue  
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 US

04-7092

ADABLE FORM:

PE: Floppy disk

IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: US/08/741,881  
 APPLICATION NUMBER: US/08/741,881  
 FILING DATE: 30-OCT-1996  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: McMaisters, David D.  
 REGISTRATION NUMBER: 33,963  
 REFERENCE/DOCKET NUMBER: 930049.42306 / 1146.007  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (206) 622-4900  
 TELEFAX: (206) 682-6031  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 16656 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 US-08-741-881-1

Query Match 56.1%; Score 3578.4; DB 1; Length 16656  
 Best Local Similarity 88.9%; Pred. No. 0;  
 Matches 4141; Conservative 0; Mismatches 16; Indels 503;

QY 1750 GAGCTCCAGCTTTTCTGAGCGGAAAGAACCCAGCTGGGGCTCTAGGGGGTATCC  
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[illegible]

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Db	14170	TTTTCACTCGGAAACCTGTGTGCCAGCTGCAATTAATGAAATCGGCCAACGGC	14229
Qy	4416	AGCGGTTTTGCGTATTGGCGCTCTTTCGCTTTCCTCGCTCACTGACTCGCTGCG	4475
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Qy	5736	ATTCAAGCTCCGGTTCCCAACGATCAAGGGCAGATTACATCATCCCCCATGTTGTG
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Qy	6096	ATCCAGTTGATTAACCCACTCGTGACCCCACTGATCTTCAAGCATCTTTTAC
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RESULT 8  
US-08-739-158-1  
Sequence 1, Application US/08739158  
Patent No. 5814482  
GENERAL INFORMATION:  
APPLICANT: Dubensky Jr, Thomas W  
APPLICANT: Polo, John M.  
APPLICANT: Jolly, Douglas J.  
APPLICANT: Driver, David A.  
TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEM  
NUMBER OF SEQUENCES: 128  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/739,158  
FILING DATE: 30-OCT-1996  
CLASSIFICATION: 514



Db	12711	TC	CCGCCCCCATGGCTGACTAAATTTTATTTATTTATATGACAGGCCGAGGCCGCC	12773
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Qy	2648	C	-----GATCAAGACACAGGATGAGG	2676
Db	12831	CT	CCGGGAGCTTGTATATCCATTTTCGGATCTGATCAAGACACAGGATGAGG	12868
Qy	2676	CG	ATGATTGAAACAAGTAGATTGCACGACGAGTTCTCCGGCCGCTTTGGTGGAG	2735
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Db	13551	GAC	ATAGCTTGCTACCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCT	13610
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Db	13611	TT	CCTCGTCTTTACCGGTATCGGCTCCCGATTGCGACGCGATCGCCTTCTAT	13670
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Db	13671	CT	TGAAGGTTCTTCTGAGCGGAGCTCTGGGGTTCGAAATGACCAACGAGA	13730
Qy	3516	AC	TGCCATCAAGATTTTCAATTCACCGCCGCTTCTTGAAGGTTGGGCT	3576
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515: GGTTCGCGCACATTTCCCGGAAAAGTGCCACCTGACGTC 16189

16 1
1. Application US/08739167
2. 1.83723
3. INFORMATION:
ICAT: Dubensky Jr, Thomas W
ICAT: Polo, John M.
ICAT: Ibanez, Carlos E.
ICAT: Chang, Stephen M.W.
ICAT: Jolly, Douglas J.
ICAT: Driver, David A.
ICAT: Belli, Barbara A.
3. OP INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTEMS AND ALPHAVIRUS
3. OP SEQUENCES: 128
3. OP SEQUENCE ADDRESS:
RES: SEED AND BERRY LLP
RES: 6300 Columbia Center, 701 Fifth Avenue
CY: Seattle
ATE: Washington
INT: US
P: 18:04-7092
3. OP READABLE FORM:
DIOP TYPE: Floppy disk
DIOP TYPE: IBM PC compatible
3. OP SYSTEM: PC-DOS/MS-DOS
3. OP RELEASE: Patent In Release #1.0, Version #1.25
3. OP APPLICATION DATA:
3. OP APPLICATION NUMBER: US/08/739,167
3. OP DATE: 30-OCT-1996
3. OP APPLICATION: 435
3. OP INFORMATION:
3. OP AGENT: McMasters, David D.
3. OP AGENT NUMBER: 33,963

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/ REFERENCE/DOCKET NUMBER: 930049.423C7 / 1146.008
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16656 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ US-08-739-167-1

Query Match      56.1%; Score 3578.4; DB 2; Length 16656
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Matches 4141; Conservative 0; Mismatches 16; Indels 503; gaps 5;

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Qy 4536 ATCAGGGGATACCGAGGAAAGACATGTGAGCAAAAGGCGAGCAAAAGGCGAG  
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Db 14470 AAATCGACGCTCAAGTCAAGGTTGGCAAAACCGACAGGACTATAAGATACCA  
Qy 4716 TCCCGCTGGAGCTCCCTCGTGGCTCTCTGTTTCCGACCTCGGCTTACCGG  
Db 14530 TCCCGCTGGAGCTCCCTCGTGGCTCTCTGTTTCCGACCTCGGCTTACCGG

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mail: watsonrj@agr.gc.ca.
Location/Qualifiers
1. .917
/organism="Gibberella zeae"
/mol_type="mRNA"
/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg08_09a03"
/tissue_type="Mycelium"
/dev_stage="Asexual"
/lab_host="E. coli DH10B"
/clone_lib="Fg08_AAPC_ECORC_Fusarium_graminearum_complex_s
ubstrate"
/notes="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."
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atc 13.9%; Score 885.2; DB 14; Length 917;  
Cal Similarity 99.7%; Pred. No. 4.6e-131;  
8 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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91. CGCTTACCATCTGCCCCAGTCTGCAATGATACCGCGAGACCCAGCTCACCGGCTCCA 858  
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554. GATTATACGAAATAACCCAGCGCGGAAGCGCGAGCGCAGAGTGTCTTGCAACT 5601  
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79. TTATCGCCCTCCATCCAGTCTATTATTTGTCGGGAAGCTAGAGTAAGTAGTTCGCCA 738  
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566. GTTAATAGTTTGGCGCAACGTTGTGCCATTGCTACAGGCATCGTGGTGTCAAGCTCGTCG 5721  
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67. TTGGTATGGCTTCATTCAGCTCCGGTCCCAACGATCAAGGCGAGTTACATGATCCCC 618  
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578. ATGTTGTGCAAAAAGCGGTAGCTCTTCGGTCTCCGATCGTGTGTGAGAAAGTTG 5841  
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584. GCGCAGTGTATCACTCATGTTATGGCAGCACTGCATAATTCTCTTACTGTGTCATGCCA 5901  
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590. TCGTAAAGATGCTTTTCTGTGACTGTGTAGTACTCAACCAAGTCATTCTGAGAAATAGTGT 5961  
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37. AATCTTTAAAGTGTCTCATCTTGGAAACGTTCTTCGGGGGGAACCTCTCAAGGATC 318  
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608. TTACCGCTGTGAGATCCAGTTCGATGTAAACCACTCGTGCAACCACTGATCTTCAGCA 6141  
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31. TTACCGCTGTGAGATCCAGTTCGATGTAAACCACTCGTGCAACCACTGATCTTCAGCA 258  
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614. TCTTTTACTTTTACAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAA 6201  
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25. TCTTTTACTTTTACAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAA 198  
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620. AAGGGAATAAGGGCGACACGGAATGTTGAATACTCATCTCTTCTCTTCAATATTAT 6261  
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Db 197 AAGGGAATAAGGGCGACACGGAATGTTGAATACTCATACTCTTCTTTTCA 138
QY 6262 TGAAGCATTTTATCAGGTTTATTGTCTCATGAGCGGATACATATTGGAATGTAT 6321
Db 137 TGAAGCATTTTATCAGGTTTATTGTCTCATGAGCGGATACATATTGGAATGTAT 78
QY 6322 AATAAACAATAAGGGTTCCGCGCACATTTCCCGGAAAAGTGCCACCTGA 63
Db 77 AATAAACAATAAGGGTTCCGCGCACATTTCCCGGAAAAGTGCCACCTAA 28
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Search completed: July 16, 2004, 00:38:23  
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2995 996 bp DNA linear GSS 22-SEP-2003  
Bc0004E12f ZMBBc (EcoRI) Zea mays subsp. mays genomic clone  
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2995.1 GI:34336220

mays subsp. mays (maize)

mayes subsp. mayes  
lycea; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
matophyta; Magnoliopsida; Lillopsida; Poales; Poaceae; PACCAD  
e; Panicoideae; Andropogoneae; Zea.  
bases 1 to 996)  
ti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,  
ard, K., Fuks, G., Yu, Y., Wing, R., and Messing, J.  
encing of the maize genome at PGIR (2003b)

act: Bharti, A. K.

acc: BUREAU, A.K.  
oachim Messing's lab

Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
ersity  
Frelinghuysen Road, Piscataway, NJ 08854, USA

732 445 5601  
732 445 5735

1: bharti@waksman.rutgers.edu

I: DnaCCTC@w  
primer: T7

S: BAC ends

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FEATURES
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Matches 908; Conservative	0; Mismatches 7; Indels 0;
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Db	142 CCACACAACATACGACCGGAAGCATAAAGTGTAAAGCCTGGGTGCCCTAAATGA
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Db	202 TAACTCACATTAATTTGGTTTGGCTCACTGCCCGCTTTCAGTCCGGGAAACCTG
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Qy	4741 TCTCCTGTTCGACCTTCGCGCTTACCGGATACCTGTTCGCGCTTTCCTCCCTTCG
Db	622 TCTCCTGTTCGACCTTCGCGCTTACCGGATACCTGTTCGCGCTTTCCTCCCTTCG
Qy	4801 GTGGCGCTTCTCATAGCTCACGCTGTAGTATCTCAGTTTCGGGTGTAGGTTCGTT
Db	682 GTGGCGCTTCTCATAGCTCACGCTGTAGTATCTCAGTTTCGGGTGTAGGTTCGTT
Qy	4861 AAGCTGGGCTGTGTGCACGAAACCCCGCTTTCAGCCCGACCGCTGCGGCTTATCC
Db	742 AAGCTGGGCTGTGTGCACGAAACCCCGCTTTCAGCCCGACCGCTGCGGCTTATCC
Qy	4921 TATCGTCTTCGATGCTCAACCCGGTAAGACACGACTTATCGCACCTGGCAGCAGCC
Db	802 TATCGTCTTCGATGCTCAACCCGGTAAGACACGACTTATCGCACCTGGCAGCAGCC
Qy	4981 AACAGGATATGACAGCGAGGTATGTAGGCGGTGCTACAGATTTCTTGAAGTGG
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Q1 1261: CCACACAAATAGGACCGGAGCAATAAGTGTAAAGCTTGGGTGCTTAAATGAGTACG 4320
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Q1 156: CAGTGTAGCAAAAGGCGCAGCAAAAGGCGCAGCAACCGTAAAGAGCGCGCTTGTGCGCTT 4619
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D1 62: CTCTCTGTTCCGACCGCTTACCGGATACCTGTCGCGTTTCTCCCTTCGGGAAG 680
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D1 86: TAAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCCTGAAAGTGGTGGCC 920
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D1 98: CTTCGG-AAAAAGAGTTGGTAGAGTCTTGTATCCGGCAACAAACC 1025

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CK287930
LOCUS
DEFINITION
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normalized, full-length Nicotiana benthamiana cDNA clone
end. mRNA sequence.
CK287930
CK287930.1 GI:39864940
Nicotiana benthamiana
Nicotiana benthamiana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE
1 (bases 1 to 910)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B
Staakavicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST750653
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
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/tissue type="abiotic and biotic stress-treated
callus tissue and root tissue"
/lab host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2:
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid
grown plants, heat-stressed leaves (38 C, 3 hr
cold-stressed leaves (5 C 3 hr, 6hr), and patho
challenged leaves (Pseudomonas syringae pv toma
Xanthomonas campestris pv campestris 12 hr, 18h
Pseudomonas syringae pv phaseolicola 18hr, and
campestris pv vesicatoria 18hr). RNA was isolat
these tissues and pooled in approximately equal
amounts."
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Query Match 14.2%; Score 903.8; DB 14; Length 910;
Best Local Similarity 99.8%; Pred. No. 5e-134;
Matches 905; Conservative 0; Mismatches 2; Indels 0;
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D1 184 AGACGAGCAGCGCGCTATCGTGGTGGCCACGACGGCGCTTCTTGGCGAGC
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521: AGGGGACACGGAATGTTGAATCATCTCTCTTTTCAATATTTGAAGCAT 6270
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3: 3' mRNA sequence.
(234786
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3: 3'
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5: Nicotiana benthamiana
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7: Eumatiophyta; Magnoliophyta; eudicotyledons; core eudicots;
8: Asterids; Lamiales; Solanales; Solanaceae; Nicotiana.
9: Bases 1 to 935)
10: Eick, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
11: Skaskawicz, B., Jin, H. and Baker, B.
12: Generation of EST sequences from Nicotiana benthamiana
13: Unpublished (2003)
14: Contact: Robin Buell
15: The Institute for Genomic Research
16: 12 Medical Center Dr, Rockville, MD 20850, USA
17: Email: potato-array@tigr.org
18: Clones can be requested from TIGR via potato@tigr.org
19: Seq primer: ATG TAG GTG ACA CTA TAG.
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32: supplier: RNA was isolated from Nicotiana benthamiana
33: tissues that include callus, roots from liquid culture
34: grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
35: cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
36: challenged leaves (Pseudomonas syringae pv tomato 12 hr;
37: Xanthomonas campestris pv campestris 12 hr, 18hr;
38: Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
39: campestris pv vesicatoria 18hr). RNA was isolated from
40: these tissues and pooled in approximately equal molar

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 8281  
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 erella zeae  
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 bases 1 to 973)  
 on, R.J., Heys, R.C., Chapados, J., Couroux, P., Harris, L.J.,  
 ori, J., Lacroix, C., Ouellet, T., Robert, L.S., Singh, J.A.,

**TITLE**  
 JOURNAL  
 COMMENT

Sprott, D. and Tinker, N.A.  
 A cDNA library prepared from Fusarium graminearum grown  
 complex plant substrate  
 Unpublished (2003)  
 Contact: Watson, Robert.J.  
 Eastern Cereal and Oilseed Research Centre  
 Agriculture and Agri-food Canada  
 Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1  
 CANADA  
 Tel: (613) 759-1655  
 Fax: (613) 759-1701  
 Email: watsonrj@agr.gc.ca.

**FEATURES**  
 source

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## ORIGIN

Query Match 14.4%; Score 915.8; DB 14; Length 973;  
 Best Local Similarity 98.6%; Pred. No. 6e-136;  
 Matches 928; Conservative 5; Mismatches 7; Indels 1;

QY 5431 TCATCCATAGTGTGCTGACTCCCGTCTGTGTAGATAACTACGATACGGAGGGC  
 Db 965 TCATCCATAGTGTGCTGACTCCCGTCTGTGTAGATAACTACGATACGGAGGGC  
 QY 5491 TCTGCGCCCGTGTGCTGCTAATGATACCGCGAGACCCACCGCTCACCGGCTCCAGT  
 Db 906 TCTGCGCCCGTGTGCTGCTAATGATACCGCGAGACCCACCGCTCACCGGCTCCAGT  
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 QY 5671 TTGCGCAACGTTGTGCCATTTGCTACAGGCGATCGTGGTGTACCGCTCGTGT  
 Db 726 TTGCGCAACGTTGTGCCATTTGCTACAGGCGATCGTGGTGTACCGCTCGTGT  
 QY 5731 GCTTCATTGAGTCTCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCGCATC  
 Db 666 GCTTCATTGAGTCTCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCGCATC  
 QY 5791 AAAAAAGCGTTAGTCTCTCGTCTCTCGATCGTTGTGTCAGAGTAAAGTTGGC  
 Db 606 AAAAAAGCGTTAGTCTCTCGTCTCTCGATCGTTGTGTCAGAGTAAAGTTGGC  
 QY 5851 TTATCACTCATGTTATGCGGAGCACTGCAATATTTCTTACTGTGTCATGCGCATCC  
 Db 546 TTATCACTCATGTTATGCGGAGCACTGCAATATTTCTTACTGTGTCATGCGCATCC  
 QY 5911 TGTCTTTCTGTGACTGTGTGAGTACTCAACCAAGTCAATCTGAGATAGTGTATC  
 Db 486 TGTCTTTCTGTGACTGTGTGAGTACTCAACCAAGTCAATCTGAGATAGTGTATC  
 QY 5971 CGGAGTTGCTCTTGGCGGCGTCAATACGGGATATACGGCGGCACATAGCAGT  
 Db 426 CGGAGTTGCTCTTGGCGGCGTCAATACGGGATATACGGCGGCACATAGCAGT



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/lab_host="E. coli DH10B"
/clone_lib="Anopheles gambiae immune competent 4A3A"
/notes="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from
forward priming site which reads from the 3' end of the
cDNA. The 4A3A is a directionally cloned and normalized
cDNA library that was constructed from the 4A3A cell line
oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
(1996) : Normalization and Subtraction: Two approaches To
Facilitate Gene Discovery, Genome Research 6, 791-806."

14.5%; Score 925.6; DB 9; Length 1004;
Best Local Similarity 99.1%; Pred. No. 1.6e-137;
Matches 925; Conservative 1; Mismatches 1; Indels 7; Gaps 7;

158C AAAAGGCCAGGAAACCGTAAAGAGCGCGTCTGCTGCGGTTTTCATAGGCTCCGCCCCC 4639
160C 1 AAAAGGCCAGGAAACCGTAAAGAGCGCGTCTGCTGCGGTTTTCATAGGCTCCGCCCCC 60
164C 1 GACGAGCATCACAATAATCGACGCTCAAGTCAGAGTGCGGAAACCGGACGAGCTACT 4699
166C 1 GACGAGCATCACAATAATCGACGCTCAAGTCAGAGTGCGGAAACCGGACGAGCTACT 120
170C AAAAGATACAGGCGTTTCCCTCGAAGCTCCCTGCTGCGGCTCTCTGTTCCGACCCCTGC 4759
172C 1 AAAAGATACAGGCGTTTCCCTCGAAGCTCCCTGCTGCGGCTCTCTGTTCCGACCCCTGC 180
176C 1 GCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCT 4819
178C 1 GCTTACCGGATACCTGTCGCGCTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCT 240
182C 1 GCGGTGTAGGTATCTCAGTTCGGTGTAGTTCGGTTCGCTCCAAGCTGGGCTGTGTCAG 4879
184C 1 GCGGTGTAGGTATCTCAGTTCGGTGTAGTTCGGTTCGCTCCAAGCTGGGCTGTGTCAG 300
188C 1 AACCCCGGTTGAGCGCGGCTGCGCTTATCGGTAACTATGCTGTGAGTCAACC 4939
190C 1 AACCCCGGTTGAGCGCGGCTGCGCTTATCGGTAACTATGCTGTGAGTCAACC 360
194C 1 GGTAAAGACACACTTATCCCACTGGCAGCAGCACTGTAACAGGATTAGCAGGCA 4999
196C 1 GGTAAAGACACACTTATCCCACTGGCAGCAGCACTGTAACAGGATTAGCAGGCA 420
200C 1 GTATGTAGCGGTGCTACAGAGTTCCTGAAGTGGTGGCTAACTACGCTACACTAGAA 5059
202C 1 GTATGTAGCGGTGCTACAGAGTTCCTGAAGTGGTGGCTAACTACGCTACACTAGAA 480
206C 1 GAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAGAGTTGTA 5119
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212C 1 GCTTGTATCCGGCAAAACCAACCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 5179
214C 1 GCTTGTATCCGGCAAAACCAACCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600
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220C 1 GAATTAACGGCAGAAAAAAGGATCTCAAGAGATCTTTTGAATCTTTTCTACGGGGCTG 660
224C 1 AGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTTGGTCAATGATATCAAAAGGA 5299
226C 1 AGCTCAGTGGAAACGAAACTCAGCTTAAGGATTTTGGTCAATGATATCAAAAGGA 720
230C 1 TTTCACCTAGATCTTTTAAATTAAGGATTTTAAATCAATCTAAAGTATATATG 5359
232C 1 TTTCACCTAGATCTTTTAAATTAAGGATTTTAAATCAATCTAAAGTATATATG 780
236C 1 ATAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACTATCTCAGCGATCT 5419
238C 1 ATAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACTATCTCAGCGATCT 839
242C 1 GTCTATTTGTTCCATCCTAGTTGCTGCTCCCGTCTGCTGATAGTAATACGATACGGG 5479

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Db      840  GTCTATTTCGTTTCATCCATAGTTGCTGACTCCCGTCTGTAGAT-ACTACGA-898
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Db      899  AGGGCTTACCATTCTGG-CCCAAGTCTGCAATATACCGGAG-CCACGCTCA-899
Qy      5540  CAGATTTCAGCATAAATAACAGCCAGCCGGAAGGCGGAGCGGAGGAGAGT 55
Db      956  CAGATTTCAGCATAAATAACAGCCAGCCGGAAGGCGGAGCGGAGGAGAGT 10

RESULT 7
CK298208 947 bp mRNA linear EST
LOCUS EST760922 Nicotiana benthamiana mixed tissue cDNA library: 2003
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone
end, mRNA sequence.
ACCESSION CK298208.1 GI:39885354
VERSION CK298208
KEYWORDS Nicotiana benthamiana
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 947)
AUTHORS Buell C.R., Hart A., Zismann V., Karameycheva S.A., Day B,
Staskiewicz B., Jin H. and Baker B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other ESTs: EST760923
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
Location/Qualifiers
1..947
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
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/tissue_type="abiotic and biotic stress-treated"
callus tissue and root tissue"
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/clone_lib="Nicotiana benthamiana mixed tissue"
library, normalized, full-length"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid
grown plants, heat-stressed leaves (38 C, 3 hr, 12),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv
Pseudomonas campestris pv campestris 12 hr, 18h
Pseudomonas syringae pv phaseolicola 18hr, and
campestris pv vesicatoria 18hr). RNA was isolated
these tissues and pooled in approximately equal
amounts."

ORIGIN
Query Match 14.5%; Score 921.4; DB 14; Length 947;
Best Local Similarity 99.4%; Pred. No. 7.8e-137;
Matches 925; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy      2681  GATTGAACAAGATGATTGACCGAGGTTCTCCGGCGCTTGGGTGGAGAGGCT-2740
Db      17 GATTGAACAAGATGATTGACCGAGGTTCTCCGGCGCTTGGGTGGAGAGGCT-2740
Qy      2741  CTATGACTGGGCACACAGCAATCGGCTGCTGTGATGCCCGCGCTTCCGGCT-2800
Db      77 CTATGACTGGGCACACAGCAATCGGCTGCTGTGATGCCCGCGCTTCCGGCT-2800

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1124 1089 bp mRNA linear EST 30-JUL-2002  
1124 Oncorhynchus mykiss Kidney infected by infectious  
-opoletic necrosis virus Oncorhynchus mykiss cdna clone KG'12,  
sequence.  
1124  
1124.1 GI:6431472  
chynchus mykiss (rainbow trout)  
chynchus mykiss  
ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
lopterygii; Neopterygii; Teleostei; Euteleostei;  
acanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.  
ases 1 to 1089)  
.T., Sakai,M. and LaPatra,S.E.  
ssed Sequence Tag Analysis of Kidney and Gill tissues from  
ow Trout (Oncorhynchus mykiss) Infected with Infectious  
opoletic Necrosis Virus  
Biotechnol. 2 (5), 493-498 (2001)  
act: Masahiro Sakai  
lty of Agriculture  
zaki University  
ishi gakuenkibandai, Miyazaki, Miyazaki 889-2192, Japan  
l: m.sakai@cc.miyazaki-u.ac.jp.  
Location/Qualifiers  
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/clone lib="Oncorhynchus mykiss Kidney infected by  
infectious hematopoietic necrosis virus"  
/note="common name:rainbow trout ; infected by infectious  
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TTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGAAGCTCAAGTCAGAGG 557

4678 TGGCGAAACCGCAGGACTATTAAGATACGAGCGTTTCCCTTGGAGCTCC  
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4738 CGCTCTCTCTGTTCGACCCCTGCGGCTTACCGGATACCTGTCCGCTTTCCTCT  
618 CGCTCTCTCTGTTCGACCCCTGCGGCTTACCGGATACCTGTCCGCTTTCCTCT  
4798 AGCGTGGCGCTTCTCATAGCTACGCTGTAGGTATCTCAGTTCCGTTAGGTCT  
678 AGCGTGGCGCTTCTCATAGCTACGCTGTAGGTATCTCAGTTCCGTTAGGTCT  
4858 TCCAAGCTGGGCTGTGTGACGACAAACCCCGTTTCAGCGCGACCTGCGCTTGA  
738 TCCAAGCTGGGCTGTGTGACGACAAACCCCGTTTCAGCGCGACCTGCGCTTGA  
4918 AACTATCGTCTTGAGTCCAAACCCCGTTTCAGCGACACTTATGCGCACTGGCAGCA  
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4978 GGTAAACAGGATTAGCAGAGCGGATGTAGGCGGTGCTACAGAGTTCTTGAAG  
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5037 GCCTTAACCTAGCGCTACACTAGAACAGAGTATTTGGTATCTGCGCTCTGCTGAA  
918 GCCTTAACCTAGCGCTACACTAGAACAGAGTATTTGGTATCTGCGCTCTGCTGGA  
5097 TACCTTCGGAAGAGTGTGAGTCTT-GATCCGGCAACAAACCA---CCG  
978 TACCTTCGGAAGAGTGTGAGTCTTCTGATCCGGCAACAAACCAACCGCT  
5153 GCGGTGTTTGTGTTGTTGCAAGCA-CCAGTTACGCGCGCAAAAAAAGAT 5  
1038 GGGGGTGTCTTTTGTGTTGCAAGCAGCAGATTACCCCGCAAAAAAAGCGAT 1  
RESULT 6  
AJ281480  
LOCUS  
DEFINITION  
4A3A-P4G8-F Anopheles gambiae immune competent 4A3A Anop  
gambiae cdna clone 4A3A-P4G8, mRNA sequence.  
ACCESSION  
AJ281480  
VERSION  
AJ281480.1 GI:6929360  
KEYWORDS  
EST.  
SOURCE  
Anopheles gambiae (African malaria mosquito)  
Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Ptery  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea  
Anopheles.  
REFERENCE  
1 (bases 1 to 1004)  
Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Robe  
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., S  
and Kafatos, F.C.  
Anopheles gambiae pilot gene discovery project: identifi  
mosquito innate immunity genes from expressed sequence t  
generated from immune-competent cell lines  
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)  
20300950  
MEDLINE  
PUBMED  
10841561  
COMMENT  
Contact: Dimopoulos G  
Fotis C. Kafatos laboratory  
European Molecular Biology Laboratory  
Meyerohofstrasse 1, 69117 Heidelberg, Germany.  
Location/Qualifiers  
1. .1004  
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67	AGCGTGGCGCTTCTCATAGCTCAACGCTGTAGGTATCTCAGTTCGGTGTAGGTTCGTCG	736
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73	TCCAAGCTGGCTGTGTGCACAAACCCCGCTTACGCCGCGCTGCGCTTATCCGGT	796
191	AACATCTGCTTGTAGTCCAAACCGGTAAAGACAGCTTATCGCCACTGGCAGCCACT	4977
79	AACATCTGCTTGTAGTCCAAACCGGTAAAGACAGCTTATCGCCACTGGCAGCCACT	856
197	GTAAACAGATTAGCAGCGGAGGTATGTAGCGGTGTACAGATCTTGAAGTGTGG	5037
85	GTAACAGATTAGCAGCGGAGGTATGTAGCGGTGTACAGATCTTGAAGTGTGG	916
203	CTAACTACGGCTTAACTAGAGGACAGTATTGGTATCTCGGCTCTGCTGAAGCCAGTT	5097
91	CTAACTACGGCTTAACTAGAGGACAGTATTGGTATCTCGGCTCTGCTGAAGCCAGTT	976
209	ACTTCGGAAGAAAGAGTGGTAGCTTCTTGATCCCGCAAAACACACCGCTGTAGCGGT	5157
97	ACTTCGGAAGAAAGAGTGGTAGCTTCTTGATCCCGCAAAACACACCGCTGTAGCGGT	1035
315	GTTTCTTTTGTTCGAACGACAGATTACGGC	5190
203	TTTTCTTTTGTTCG-AGCAGCAGATTACGGC	1067
RE	U	
CK	8	
LC	10	
DE	11	
AC	E	
VE	S	
KE	W	
SO	R	
RE	E	
CT		
OT		
CO	MI	
FE	TI	

67	ASCGTGGCGCTTCTCATAGCTCAACGCTGTAGGTATCTCAGTTCGGTGTAGTGTGCG	736
185	TCCAAGCTGGCTGTGTGACGAACCCCGCTTTCAGCCGCGCGCTTATCCGGT	4917
73	TCCAAGCTGGCTGTGTGACGAACCCCGCTTTCAGCCGCGCGCTTATCCGGT	796
191	ATCTATCGTTCGAGTCCAAACCGGTAAGACAGCACTTATCGCACTGGCAGAGCACT	4977
79	ATCTATCGTTCGAGTCCAAACCGGTAAGACAGCACTTATCGCACTGGCAGAGCACT	856
197	CTAAACAGATTTAGCAGAGCGAGTATGTAGCGGTGTACAGAGTCTTGAAGTGTGG	5037
85	CTAAACAGATTTAGCAGAGCGAGTATGTAGCGGTGTACAGAGTCTTGAAGTGTGG	916
103	CTAACTACGGCTACACTAGAGAAACAGTATTGGTATCTGGCGCTCTGTGAAGCCAGT	5097
91	CTAACTACGGCTACACTAGAGAAACAGTATTGGTATCTGGCGCTCTGTGAAGCCAGT	976
109	ATCTCGGAAGAGTGTGTAGCTTTCATCGCGCAACAAACACCGCTGTAGCGGT	5157
97	ATCTCGGAAGAGTGTGTAGCTTTCATCGCGCAACAAACACCGCTGTAGCGGT	1035
115	GTCTTTTGTGTGCAAGCAGCAGATTACGCGC 5190	
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C 233361 954 bp mRNA linear EST 15-DEC-2003  
 F T46083 Nicotiana benthamiana mixed tissue cDNA library,  
 normalized, full-length Nicotiana benthamiana cDNA clone NBMAG50 5'  
 e.d. mRNA sequence.  
 C 233361  
 C 233361.1 GI:39855898  
 E T  
 N cotiana benthamiana  
 E cotiana benthamiana  
 E karyocya, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 e eumatiophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 a torids; lamids; Solanales; Solanaceae; Nicotiana.  
 E eil.C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,  
 Caskawicz, B., Jin, H. and Baker, B.  
 C generation of EST sequences from Nicotiana benthamiana  
 C published (2003)  
 C Her ESTs: EST746084  
 C n'act: Robin Buell  
 I e Institute for Genomic Research  
 9 23 Medical Center Dr, Rockville, MD 20850, USA  
 3 ail: potato-array@tigr.org  
 C ones can be requested from TIGR via potato@tigr.org  
 S q primer: ATT TAG GTG ACA CTA TAG.  
 Location/Qualifiers  
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 tissues that include callus, roots from liquid culture  
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 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen  
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;  
 Xanthomonas campestris pv campestris 12 hr, 18hr;  
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas  
 campestris pv vesicatoria 18hr). RNA was isolated from

these tissues and pooled in approximately equal amounts."

1137 1067 bp mRNA linear EST 30-JUL-2002  
1137 Oncorhynchus mykiss Kidney infected by infectious  
topoietic necrosis virus Oncoirhynchus mykiss cDNA clone KI2,  
, sequence.  
1137  
1137.1 GI:6431485  
rhynchus mykiss (rainbow trout)  
rhynchus mykiss

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostei; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus (bases 1 to 1067)	
Kono, T., Sakai, M. and LaPatra, S.E. Expressed Sequence Tag Analysis of Kidney and Gill Tissue of Rainbow Trout ( <i>Oncorhynchus mykiss</i> ) Infected with Infectious Hematopoietic Necrosis Virus	Mar. Biotechnol. 2 (5), 493-498 (2001)
Contact: Masahiro Sakai Faculty of Agriculture Miyazaki University 1-1 nishi gakuentsibanadai, Miyazaki, Miyazaki 889-2192, Japan Email: m.sakai@cc.miyazaki-u.ac.jp	

## FEATURES

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i.: : : 1087,
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infectious hematopoietic necrosis virus"
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## ORIGIN

Query Match	15.0%;	Score 954.6;	DB 9;	Length 1067;
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Matches 982;	Conservative 0;	Mismatches 9;	Indels 2;	
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Db	137	ATTCCACACAATACGAGCGGAAGCATAAAGTGTAAGAGCCTCGGGGTCCCTAA		
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Db	197	AGCTAACTCACATTAATTCGGTTTCGCTCACTGCCCGCTTCCAGTCGGGAAC		
Qy	4378	TGCGAGCTGCATTAATGMAATCGGCCAAACGCGGGGAGAGGCGGTTTTCGCTAT		
Db	257	TGCGAGCTGCATTAATGMAATCGGCCAAACGCGGGGAGAGGCGGTTTTCGCTAT		
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Db	377	TCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATACGCA		
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Db	437	AACATGTGACAAAAGCCAGCAAAAGCCAGGAACCGGTAAAGAGCCGCGGTTCG		
Qy	4618	TTTTTCCATAGGCTCCGCCCCCTCGACGAGCATCACAAAAATCGACGCTCAAGT		
Db	497	TVVTTCCATAGGCTCCGCCCCCTCGACGAGCATCACAAAAATCGACGCTCAAGT		
Qy	4678	TGGCGAAACCGACAGACTATAAAGTACCAAGGCGTTTCCCGCTCGGAAGCTCC		
Db	557	TGGCGAAACCGACAGACTATAAAGTACCAAGGCGTTTCCCGCTCGGAAGCTCC		
Qy	4738	CGCTCTCTCTTCGACCCCTGCGGCTTACCGGATACCTGTCCGCCCTTCTCCCT		
Db	617	CGCTCTCTCTTCGACCCCTGCGGCTTACCGGATACCTGTCCGCCCTTCTCCCT		
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-		/note="Vector: p7T73D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized oligo-T primed cDNA according to: Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."
OR G.		
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+	at	10e%; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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QY		AATCAGAGTGCGGAACCCGACGAGACTATAAGATACCAGGCGTTTCCCCCTGGAGC 4728
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QY		CATTCCGGAAAGCGTGGCGCTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGGTAG 4848
DB		CATTCCGGAAAGCGTGGCGCTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGGTAG 240
QY		GTCGTTTCGCTCCAAAGCTGGGCTGTGTGCAGAACCCCGCTTACGCCGACCGCTGGCC 4908
DB		GTCGTTTCGCTCCAAAGCTGGGCTGTGTGCAGAACCCCGCTTACGCCGACCGCTGGCC 300
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LOCUS						
DEFINITION	BM438846	1013 bp	linear			
ACCESSION	IP1VR00157	Liver cdna library	Ictalurus punctatus cdna 5			
VERSION	sequence.					
KEYWORDS	BM438846					
SOURCE	BM438846.1	GI:18460568				
ORGANISM	Ictalurus punctatus	(channel catfish)				
REFERENCE	Feng,J., Kucuktas,H., Kocabas,A., Li,P. and Liu,Z.					
AUTHORS	Transcriptome of channel catfish (Ictalurus punctatus): a					
TITLE	analysis of expressed sequence tags from the liver					
JOURNAL	Unpublished (2002)					
COMMENT	Contact: Liu ZJ					
	The Fish Molecular Genetics and Biotechnology Laboratory					
	Department of Fisheries and Allied Aquacultures and Program					
	and Molecular Biosciences					
	Auburn University					
	203 Swingle Hall,					
	Tel: 334 844 4054					
	Fax: 334 844 9208					
	Email: zliu@acesag.auburn.edu					
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	/clone_lib="Liver cdna library"					
	/notes="Organ: Liver; Vector: pSport1; Site 1: M13					
	Site 2: SalI"					
FEATURES						
source						

[illegible]

GenCore version 5.1.6  
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leic search, using sw model

July 15, 2004, 07:32:41 ; Search time 14541 Seconds  
(without alignments)  
13092.043 Million cell updates/sec

US-10-668-496-2

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IDENTITY NUC

3apop 10.0 , Gapext 1.0

27513289 seqs, 14931090276 residues

hits satisfying chosen parameters: 55026578

ength: 0

ength: 2000000000

Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

EST:\*

1: em\_ectba:\*  
2: em\_ectum:\*  
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5: em\_ectov:\*  
6: em\_ectpl:\*  
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8: em\_ectc:\*  
9: gb\_ect1:\*  
10: gb\_ect2:\*  
11: gb\_ect3:\*  
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13: gb\_ect5:\*  
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16: em\_ectom:\*  
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19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_pbg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

is the number of results predicted by chance to have a  
ter than or equal to the score of the result being printed,  
ived by analysis of the total score distribution.

# SUMMARIES

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14.7	954	14	CK283361	CK283361 EST746083

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c 8	915.8	14.4	973	14	CD458281	CK298208
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10	907.8	14.2	936	14	CK256977	CK284786
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c 15	885.2	13.9	917	14	CD458286	CG329216
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c 17	879.4	13.8	925	14	CB686151	CK291799
c 18	872.6	13.7	935	12	BG838279	CB686151
c 19	866.6	13.6	1073	14	CF269652	BG838279
c 20	865	13.6	1073	14	CF269652	CF269652
c 21	854	13.4	1056	29	CG835880	CF269652
c 22	841	13.2	841	9	AL042026	CG835880
c 23	839.8	13.2	856	14	CK287297	AL042026
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c 26	821.2	12.9	1249	28	BZ572284	BM438950
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c 38	779.4	12.2	800	9	AJ281449	CB686421
c 39	774.8	12.2	1336	28	BZ575810	AJ281449
c 40	774.4	12.1	789	14	CD280920	BZ575810
c 41	774	12.1	954	9	AL044364	CD280920
c 42	770	12.1	1370	28	BZ571721	AL044364
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## ALIGNMENTS

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gambiae cDNA clone 4A3A-P6F11, mRNA sequence.  
ACCESSION AJ281552  
VERSION AJ281552.1 GI:6929432  
KEYWORDS EST.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Ptery  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoides  
Anopheles.  
REFERENCE 1 (bases 1 to 1070)  
AUTHORS Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Robe  
Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., S  
and Kafatos, F.C.  
TITLE Anopheles gambiae pilot gene discovery project: identifi  
mosquito innate immunity genes from expressed sequence t  
generated from immune-competent cell lines  
Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)  
JOURNAL MEDLINES 20300950  
PUBMED 10841561  
COMMENT Contact: Dimopoulos G  
Fotis C. Kafatos Laboratory  
European Molecular Biology Laboratory  
Meyerhofstrasse 1, 69117 Heidelberg, Germany.



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894 13 Application US/10395894
100 NO. US20040033229A1
INF REACTION:
NT: MADDON, Paul J.
NT: DONOVAN, Gerald P.
NT: OLSON, William C.
NT: SCHELKE, No. US20040033229Albert
NT: GARDNER, Jason
NT: VA, Dangshe
PT INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
FER NC#: P00741.70005.US
AP LIC: LICATION NUMBER: US/10/395,894
FILING DATE: 2003-03-24
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ILLG DATE: 2002-10-23
PPL CATION NUMBER: US 60/335,215
ILLG DATE: 2001-10-23
PPL CATION NUMBER: US 60/362,747
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PPL CATION NUMBER: US 60/412,618
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894 13
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Pos	ISM Artificial Sequence	RE: IN: RMATION: Plasmid	56.1%; Score 3578.4; DB 13; Length 6085;	88.9%; Prid. No. 0;	Conservative 0; Mismatches 16; Indels 503; Gaps 5;
175	Q1	AGCTCCACGCTTTTCTGAGCGGGAAGAACACAGCTGGGGCTCTAGGGGTATCCCAAGC	1809		
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181	Q2	CCCTGTAGCGCGGAGTAACGCGGGGGGTGTGGTGTATACGCGCAGCGTACCGGTAC	1869		
195	D2	CCCTGTAGCGCGCAATTAAGCGGGGGGTGTGGTGTATACGCGCAGCGTACCGGTAC	2014		
187	Q3	ACTTGCAGCGCCCTAGCGCGCGCTTCTTCCGCTTCTTCCCTTCTTCTCGGCACGTT	1929		
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210	Q7	CTGTGTCCAAATCTGGAACAACACCTCAACCCCTATCTCGGTCTATTCTTTGATTTAATAGG	2168		
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228	Q10	GAGCGGAAAGAACACAGCTGTGGAATGTGTGAGTTAGGGTGTGAAAGTCCCAAGCT	2348		
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RESULT 12  
US-10-395-894-11  
; Sequence 11, Application US/10395894  
; Publication No. US20040033229A1  
; GENERAL INFORMATION:  
; APPLICANT: MADDON, Paul J.  
; APPLICANT: DONOVAN, Gerald P.  
; APPLICANT: OLSON, William C.  
; APPLICANT: SCHLICK, No. US20040033229Albert  
; APPLICANT: GARDNER, Jason  
; APPLICANT: MA, Dangshe  
; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS  
; FILE REFERENCE: P00741.70005 US  
; CURRENT APPLICATION NUMBER: US/10/395,894  
; CURRENT FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: PCT/US02/33944  
; PRIOR FILING DATE: 2002-10-23  
; PRIOR APPLICATION NUMBER: US 60/335,215  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: US 60/362,747  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/412,618  
; PRIOR FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 6085  
; TYPE: DNA





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pplication US/10395894  
: US20040033229A1  
ATION:  
DON, Paul J.  
ONOVAN, Gerald P.  
LSON, William C.  
:ChelKE, No. US20040033229A1bert  
:ARDNER, Jason  
IA, Dangshe  
NTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS  
E: P00741.70005.US

; CURRENT APPLICATION NUMBER: US/10/395,894  
; CURRENT FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: PCT/US02/33944  
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; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: US 60/412,618  
; PRIOR FILING DATE: 2002-09-20  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 6082  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: Plasmid  
US-10-395-894-10

Query Match 56.1%; Score 3578.4; DB 13; Length 6082  
Best Local Similarity 88.9%; Pred. No. 0;  
Matches 4141; Conservative 0; Mismatches 16; Indels 503;

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[illegible][illegible]

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## RESULT 9

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; Sequence 8, Application US/10395894
; Publication No. US20040033229A1
; GENERAL INFORMATION:
; APPLICANT: MADDON, Paul J.
; APPLICANT: DONOVAN, Gerald P.
; APPLICANT: OLSON, William C.
; APPLICANT: SCHSLKE, No. US20040033229A1bert
; APPLICANT: GARDNER, Jason
; APPLICANT: MA, Dangshe
; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
; FILE REFERENCE: P00741.70005.US
; CURRENT APPLICATION NUMBER: US/10/395,894
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: PCT/US02/33944
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/335,215
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/362,747
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/412,618
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.1
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US-10-395-894-8
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Query Match 56.1%; Score 3578.4; DB 13; Length 6082
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## RESULT 7

US-09-559-874-5  
; Sequence 5, Application US/09559874  
; Publication No. US20020192726A1



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; Sequence 3, Application US/09844645
; Patent No. US20020102242A1
; GENERAL INFORMATION:
; APPLICANT: Briles, David E.
;             McDaniel, Larry S.
;             Curiel, David T.
; TITLE OF INVENTION: COMPOSITION AND METHODS FOR
;                     ADMINISTERING PNEUMOCOCCAL DNA
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curiel, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent-In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/844,645
; FILING DATE: 27-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/759,505
; FILING DATE: 04-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2450
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-844-645-3

Query Match          56.1%; Score 3578.4; DB 9; Length 5446;
Best Local Similarity 88.9%; Pred. No. 0;
Matches 4141; Conservative 0; Mismatches 16; Indels 503;

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DATE: 1998-12-07
, ID NOS: 13
entIn Ver. 2.1

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Official Sequence

**ATION: Description of Artificial Sequence: mutagen**

56.1%; Score 3578.4; DB 9; Length 5432; ilarity 89.9%; Pred. No. 0; Conservative 0; Mismatches 16; Indels 503; Gaps 5;	
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Db	1722	GAATTAATTT
Qy	2289	GAGCGGAAAGAACCAAGCTGTGGAAATGTGTGTCTAGTTAGGCGTGTGMAAGTCCCT
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Qy	2976	CAGGATCTCCTGTCTCATCTCACTTGTCTCTGCGAGAAAGTATCTCATATGCGCT
Db	2434	CAGGATCTCCTGTCTCATCTCACTTGTCTCTGCGAGAAAGTATCTCATATGCGCT
Qy	3036	ATGCGCGGCTGCATAGCTTTGATTCGGGCTACTCTGGCCATTTCGACACCAAGCGC
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Qy	3096	CGCATCGAGCGAGCAGCTATCTCGGATGGAAGCGGCTTGTCTCATCAGGATGAT
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[illegible]

RESULT 4

US-10-115-440-8

; Sequence 8, Application US/10115440

; Publication No. US20040086845A1

; GENERAL INFORMATION:

; APPLICANT: WU, Tzyy-Choon

; APPLICANT: HUNG, Chien-Fu

; TITLE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANS-

; TITLE OF INVENTION: BACTERIAL TOXIN TO AN ANTIGEN

; FILE REFERENCE: 02240-179934

; CURRENT APPLICATION NUMBER: US/10/115,440

; CURRENT FILING DATE: 2002-09-30

; PRIOR APPLICATION NUMBER: US 60/281,003

; PRIOR FILING DATE: 2001-04-04

; PRIOR APPLICATION NUMBER: PCT/US00/41422

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: US 09/501,097

; PRIOR FILING DATE: 2000-02-09

; PRIOR APPLICATION NUMBER: US 09/421,608

; PRIOR FILING DATE: 1999-10-20

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 5431

; TYPE: DNA

; ORGANISM: Plasmid pcdNA3

US-10-115-440-8

Query Match 56.1%; Score 3578.4; DB 17; Length 5431  
Best Local Similarity 88.9%; Pred. No. 0;  
Matches 4141; Conservative 0; Mismatches 16; Indels 503;

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```

RE: J. Application US/10617619  
 for No. US20040110929A1  
 INVENTOR:  
 J. B. Jorgensen, Soren E  
 J. B. Jorgensen, Anker S  
 J. B. Jorgensen, Anker S  
 J. B. Jorgensen, Anker S

FILE REFERENCE: 6455,200-US  
 CURRENT APPLICATION NUMBER: US/10/617,619  
 CURRENT FILING DATE: 2003-07-11  
 PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099  
 PRIOR FILING DATE: 2002-07-12  
 PRIOR APPLICATION NUMBER: US 60/404,568  
 PRIOR FILING DATE: 2002-08-19  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 10  
 LENGTH: 7493  
 TYPE: DNA  
 ORGANISM: Artificial  
 FEATURE:  
 OTHER INFORMATION: Synthetic  
 US-10-617-619-10

Query Match 56.2%; Score 3581.4; DB 17; Length 7493  
 Best Local Similarity 88.9%; Pred. No. 0;  
 Matches 4143; Conservative 0; Mismatches 11; Indels 505; 5:

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08:16:06 2004

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JS-10-668-496-2

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IDENTITY\_NUC

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Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
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ived by analysis of the total score distribution.

#### SUMMARIES

Query Match	Length	DB	ID	Description
56.2	6431	16	US-10-340-447-4	Sequence 4, Appli
56.2	7427	17	US-10-617-619-13	Sequence 13, Appl
56.2	7493	17	US-10-617-619-10	Sequence 10, Appl
56.1	5431	17	US-10-115-440-8	Sequence 9, Appli
56.1	5432	9	US-09-794-975-9	Sequence 9, Appli
56.1	5446	9	US-09-844-645-3	Sequence 3, Appli
56.1	5446	9	US-09-559-874-5	Sequence 5, Appli
56.1	5446	16	US-10-371-116A-1	Sequence 1, Appli
56.1	6082	13	US-10-395-894-8	Sequence 8, Appli
56.1	6082	13	US-10-395-894-9	Sequence 9, Appli
56.1	6082	13	US-10-395-894-10	Sequence 10, Appli
56.1	6085	13	US-10-395-894-11	Sequence 11, Appli
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17	3578.4	56.1	6238	15	US-10-204-310-1	Sequenc
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#### ALIGNMENTS

RESULT 1  
US-10-340-447-4  
; Sequence 4, Application US/10340447  
; Publication No. US20040002115A1  
; GENERAL INFORMATION:  
; APPLICANT: FRAISSIGNES, Pauline  
; APPLICANT: GRATZER, Sabine  
; APPLICANT: LEBERER, Ekkehard  
; TITLE OF INVENTION: METHOD OF IDENTIFYING PROTEIN CAMS (CONSTITUT  
; TITLE OF INVENTION: MUTANTS)  
; FILE REFERENCE: DEAV2002/0003 USNP  
; CURRENT APPLICATION NUMBER: US/10340,447  
; PRIOR FILING DATE: 2003-01-10  
; PRIOR APPLICATION NUMBER: DE 02000733.2  
; PRIOR FILING DATE: 2002-01-12  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 6431  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Nucleotide Sequence of pcDNA3.1(+) - Edge 5  
US-10-340-447-4

Query Match 56.2%; Score 3581.4; DB 16; Length 6431  
Best Local Similarity 88.9%; Pred. No. 0;  
Matches 4143; Conservative 0; Mismatches 11; Indels 505;  
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Db 2245 GGGCTCTATGCTTCTGAGCGGAAAGAACAGCTGGGGCTCTAGGGGGTATCC  
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Db 3378 -----  
Qy 3876 AGGCTCGCAGCCAAACGTCGGGGGGCAGGCCCTGCCATAGCCTCAGTGTCAAC  
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Qy 3936 CGATTCCACCGCCCTTCTATGAAAGTTGGGCTTCGGAATCGTTTTCGGGA  
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Qy	6276	GGGTATTTGTCTCATGACGGGATACATATTGTGAATGTAATTTAGAAAAATAACA
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Qy	6336	GGTTCCGCGACATTTTCCCGAAAGTGCCACTGACGTC 6375
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## RESULT 14

US-08-073-836-3  
Sequence 3, Application US/08073836  
Patent No. 5650306  
GENERAL INFORMATION:  
APPLICANT: Nabel, Gary J.  
APPLICANT: Yang, Zhi-yong  
APPLICANT: Liu, Jinsong  
TITLE OF INVENTION: RECOMBINANT NUCLEIC ACIDS FOR INHIBITING  
TITLE OF INVENTION: HIV GENE EXPRESSION  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CAMPBELL AND FLORES  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States of America  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/073,836  
FILING DATE: 07-JUN-1993  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-UM 9646  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5653 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
US-08-073-836-3

Query Match 56.1%; Score 3577; DB 1; Length 5653;  
Best Local Similarity 88.6%; Pred. No. 0;  
Matches 4156; Conservative 0; Mismatches 65; Indels 470;

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 QY 4236 GTGAAATTTGTTATCCGCTCACAATTCACAAACATAGAGCGGAGCATAAAC----- 4295  
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 QY 14050 GTGAAATTTGTTATCCGCTCACAATTCACAAACATAGAGCGGAGCATAAAC----- 14109  
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 QY 4296 AGCCTGGGGTCCCTTAATGAGTGAGTAACTCAATTAATTCGTTGGCTCACT----- 4355  
 DB |||||  
 QY 14110 AGCCTGGGGTCCCTTAATGAGTGAGTAACTCAATTAATTCGTTGGCTCACT----- 14169  
 DB |||||  
 QY 4356 TTTCCAGTCGCGGAAACCTGTCGTCAGCTCAATTAATGAATCGGCCAACCGCG----- 14215  
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 QY 14170 TTTCCAGTCGCGGAAACCTGTCGTCAGCTCAATTAATGAATCGGCCAACCGCG----- 14219  
 DB |||||  
 QY 4416 AGCGGTTTGGGTTATGGGCGCTCTTCGCGCTTCCTCGCTCACTGCTGCTGCG----- 14275  
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 QY 14230 AGCGGTTTGGGTTATGGGCGCTCTTCGCGCTTCCTCGCTCACTGCTGCTGCG----- 14289  
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 QY 4476 CGTTTCGCTGCGCGAGCGGCTATCAGCTCACTCAAGCGGCTAAATACGTTTATC----- 14335  
 DB |||||  
 QY 14290 CGTTTCGCTGCGCGAGCGGCTATCAGCTCACTCAAGCGGCTAAATACGTTTATC----- 14349  
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 QY 4536 ATCAGGGATTAACGCGAGAAAGAAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAG----- 14395  
 DB |||||  
 QY 14350 ATCAGGGATTAACGCGAGAAAGAAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAG----- 14409  
 DB |||||  
 QY 4596 TAAAAAGCGCGGTTGCTGGGTTTTCATAGGCTCGCGCCCTCGCCCTGACGAGCA----- 14555  
 DB |||||  
 QY 14410 TAAAAAGCGCGGTTGCTGGGTTTTCATAGGCTCGCGCCCTCGCCCTGACGAGCA----- 14549  
 DB |||||  
 QY 4656 AAATCGAGCTCAAGTCAGAGTTCGCGGAAACCCGACAGGACTATAAAGATACCA----- 14715  
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 QY 14470 AAATCGAGCTCAAGTCAGAGTTCGCGGAAACCCGACAGGACTATAAAGATACCA----- 14715  
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 QY 4716 TCCCGCTGGAGGCTTCCTGCTGCGCTCTCTGTTTCCGACCTCGCGTTTACCGG----- 14775  
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 QY 14530 TCCCGCTGGAGGCTTCCTGCTGCGCTCTCTGTTTCCGACCTCGCGTTTACCGG----- 14589  
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 QY 4776 GTCCGCTTCTCCCTTCGCGGAGCGTGGCGCTTCTCATAGCTCACTGCTGCTGAG----- 4835  
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 QY 14590 GTCCGCTTCTCCCTTCGCGGAGCGTGGCGCTTCTCATAGCTCACTGCTGAG----- 14649  
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 QY 4836 CAGTTCCGCTGTAGTTCGCTTCCGCTCAAGCTGGGCTGTGTGACGAAACCCCGCT----- 4895  
 DB |||||  
 QY 14650 CAGTTCCGCTGTAGTTCGCTTCCGCTCAAGCTGGGCTGTGTGACGAAACCCCGCT----- 14709  
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 QY 4896 CGACCGCTCGCGCTTATCCCGGTAACTATCGTTCGTTCGATCCCAACCCCGGTAAAGAC----- 14955  
 DB |||||

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|||||  
3CTCTTCCGCGCTCAATACGGGATAATACCGGCCACATAGCAGAACTTTAAAGT 15849  
|||||  
3CATCATTTGGAAGAACTTTCTTGGGGCGAAACTCTCAAGGATCTTACCGCTGTTGAG 6095  
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3CATCATTTGGAAGAACTTTCTTGGGGCGAAACTCTCAAGGATCTTACCGCTGTTGAG 15909  
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TTCCCGCACATTTCCCGGAAAGTGCCACCTGACGTC 6375  
|||||  
TTCCCGCACATTTCCCGGAAAGTGCCACCTGACGTC 16189  
|||||

olication US/09236140A

6236

SMATION:

NT: Dubensky Jr, Thomas W  
Polo, John M.  
Ibanez, Carlos E.  
Chang, Stephen M.W.  
Jolly, Douglas J.  
Driver, David A.  
Belli, Barbara A.

F INVENTION: RECOMBINANT ALPHAVIRUS PARTICLES

OF SEQUENCES: 124

DENSE ADDRESS:

DRESSEE: OPPENHEIMER WOLFF & DONNELLY

REET: 840 NEWPORT CENTER DRIVE, SUITE 700

TY: NEWPORT BEACH

ATE: CALIFORNIA

JNTRY: US

P: 92660

3 READABLE FORM:

DIUM TYPE: Floppy disk

MPUTER: IBM PC compatible

ERATING SYSTEM: PC-DOS/MS-DOS

FTWARE: Patent in Release #1.0, Version #1.25

APPLICATION DATA:

PLICATION NUMBER: US/09/236,140A

LING DATE: 22-Jan-1999

ASSIFICATION: <Unknown>

Y/AGENT INFORMATION:

ME: Cullman, Louis C.

GISTRATION NUMBER: 39,645

REFERENCE/DOCKET NUMBER: 20263.332 / 1146.020

MUNICATION INFORMATION:

LEPHONE: (949) 823.6000

LEFAX: (949) 823.6100

FOR SEQ ID NO: 1:

E CHARACTERISTICS:

NGTH: 16656 base pairs

PE: nucleic acid

RANDEDNESS: single

POLOGY: linear

E DESCRIPTION: SEQ ID NO: 1:

US-09-236-140A-1

Query Match 56.18; Score 3578.4; DB 4; Length 16656  
Best Local Similarity 88.94; Pred. No. 0;  
Matches 4141; Conservative 0; Mismatches 16; Indels 503;

Qy	1750	GAGCTCTCAGCGCTTTTCTGAGCGGGAAGAACCCAGCTGGGGCTCTAGGGGGGTATCC	
Db	11999	GGGCTCTATGGCTTCTGAGGGGGAAGAACCCAGCTGGGGCTCTAGGGGGGTATCC	
Qy	1810	GCCTGTAGCGGCGCATTAAGCGCGGCGGTGTGGTTACGCGCAGCGTGAC	
Db	12059	GCCTGTAGCGGCGCATTAAGCGCGGCGGTGTGGTTACGCGCAGCGTGAC	
Qy	1870	ACTTGCAGCGCCTAGCGCGCGCTTTCGCTTTCGCTTTCCTCCCTTCTTCGCG	
Db	12119	ACTTGCAGCGCCTAGCGCGCGCTTTCGCTTTCGCTTTCCTCCCTTCTTCGCG	
Qy	1930	CGCGCGCTTTCCTCCGCTCAAGCTCTAAATCGGGGCGC-TCCCTTTAGGGTTCCGATT	
Db	12179	CGCGCGCTTTCCTCCGCTCAAGCTCTAAATCGGGGCGC-TCCCTTTAGGGTTCCGATT	
Qy	1989	TTTACGGCACTCGACCCCAAAAACTTGATTTAGGGTGATGTTCAAGTAGTG	
Db	12239	TTTACGGCACTCGACCCCAAAAACTTGATTTAGGGTGATGTTCAAGTAGTG	
Qy	2049	GCCTGTAGTAGCGGTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCG	
Db	12299	GCCTGTAGTAGCGGTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCG	
Qy	2109	CTTGTTCCAAACTGGAAACACACTCAACCCCTATCTCGGTCTATTTCTTTGATTT	
Db	12359	CTTGTTCCAAACTGGAAACACACTCAACCCCTATCTCGGTCTATTTCTTTGATTT	
Qy	2169	GATTTTCCGATTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCG	
Db	12419	GATTTTCCGATTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCG	
Qy	2229	GATTTAATCTGTGGAATGCCCGGAGCTTGTATATCCATTTTCGGATCTGATC	
Db	12479	GATTTAATCTGTGGAATGCCCGGAGCTTGTATATCCATTTTCGGATCTGATC	
Qy	2289	GAGCGGGAAGAACACAGCTGTGGAATGTGTCTAGTTAGGGTGTGGAAGTCCC	
Db	12488	-----CTGTGGAATGTGTCTAGTTAGGGTGTGGAAGTCCC	
Qy	2349	CCCCA-GCAGCGAGAGTATGCAAGCATGCACTCTCAATTTAGTCAGCAACAGG	
Db	12531	CCCCAGCGAGCGAGAGTATGCAAGCATGCACTCTCAATTTAGTCAGCAACAGG	
Qy	2408	AAGTCCCGCGGCTCCCGCAGCGAGAGTATGCAAGCATGCACTCTCAATTTAG	
Db	12591	AAGTCCCGCGGCTCCCGCAGCGAGAGTATGCAAGCATGCACTCTCAATTTAG	
Qy	2468	ACCATAGTCCCGCGGCTTAACTCCCGCCCATCCCGCCCTTAACTCCCGCGGCTTCC	
Db	12651	ACCATAGTCCCGCGGCTTAACTCCCGCCCATCCCGCCCTTAACTCCCGCGGCTTCC	
Qy	2528	TCTCCGCGCATGGCTGACTAAATTTTTTTTTTTTATTTATGAGAGCGCGAGCGCGCC	
Db	12711	TCTCCGCGCATGGCTGACTAAATTTTTTTTTTTTATTTATGAGAGCGCGAGCGCGCC	
Qy	2588	TCTGAGCTTATCCAGAAAGTGTGAGGAGGCTTTTTTGGAGGCGCTAGGCTTTTGC	
Db	12771	TCTGAGCTTATCCAGAAAGTGTGAGGAGGCTTTTTTGGAGGCGCTAGGCTTTTGC	
Qy	2648	C-----CATCAAGAGACAGGATGAGGA	
Db	12831	CTCCCGGAGCTTGTATATCCATTTTCGGATCTGATCAAGAGACAGGATGAGGA	
Qy	2676	CGCATGATTGACAGAGATGGAATTCACGAGGTTTCTCGGCGCGCTTGGGTGGAG	
Db	12891	CGCATGATTGACAGAGATGGAATTCACGAGGTTTCTCGGCGCGCTTGGGTGGAG	



POLOGY: linear  
3 DESCRIPTION: SEQ ID NO: 1:

56.1%; Score 3578.4; DB 4; Length 16656;  
ilarity 88.9%; Pred. No. 0;  
Conservative 0; Mismatches 16; Indels 503; Gaps 5;  
3CTCAGCTTTCTGAGGCGGAAAGAACAGCTGGGGCTCTAGGGGGTATCCCCAGC 1809  
|||  
3CTCTATGGCTTTCTGAGGCGGAAAGAACAGCTGGGGCTCTAGGGGGTATCCCCAGC 12058  
|||  
CTGTAGCGGCGCATTAAGCGCGGGGTGTGTGTACGCGCAGCGTGACCGCTAC 1869  
|||  
CTGTAGCGGCGCATTAAGCGCGGGGTGTGTGTACGCGCAGCGTGACCGCTAC 12118  
|||  
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|||  
TTGCCAGGCGCGCTAGCGCGCGCTCTCTTCGCTTCTTCCTTCCTTCCTTCGCGCAAGTT 12178  
|||  
CGGCTTTCCCGGTCAAGCTCTAAATCGGGC-TCCCTTTAGGGTTCCGATTTAGTGC 1988  
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-----CTGTGGAAATGTGTCTCAGTTAGGGTGTGGAAAGTCCCGAGCT 12530  
|||  
CCA-GCAGGAGAGATATCAAAAGCATGCTCTCAATTAGTCAGCAACCAAGGTGTGGA 2407  
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GTCCGAGGCTCCCGAGGAGGAGATATGCAAAAGCATGCTCTCAATTAGTCAGCA 12650  
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CATAGTCCGCGCCCTAACTCCGCGCATCCGCGCCCTAACTCCGCGCATCCGCGCCAT 2527  
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TCGCGCCCATGGCTGATTAATTTTATTTATGAGAGGCGGAGCGCGCTTCGCGCC 12770  
|||  
TGAGCTATTCAGAGTAGTAGGAGGCTTTTGGAGGCTTAGGCTTTTGGAGAT 2647  
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|||  
-----GATCAAGAGACAGGATGAGGATCGTTT 2675  
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CCCGGAGGCTTGATATCAATTTTCGATCTGATCAAGAGACAGGATGAGGATCGTTT 12890  
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Db 12891 CGCATGATTGAACAAGATGATTGCAACGAGTTTCTCCGCGCGCTTGGGTGGAG  
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Qy 2736 TTGGCTATGATCGGGCAACAAGCAATCGGCTGCTCTGATCGCGCGCTGTTTC  
|||  
Db 12951 TTGGCTATGATCGGGCAACAAGCAATCGGCTGCTCTGATCGCGCGCTGTTTC  
|||  
Qy 2796 TCAGCGCAGGGCGCGCGCTTCTTTTGTCAAGACCGACCTGTCCGGTGCCTG  
|||  
Db 13011 TCAGCGCAGGGCGCGCGCTTCTTTTGTCAAGACCGACCTGTCCGGTGCCTG  
|||  
Qy 2856 CTGCAAGACGAGGCGCGCTATCGTGGCTGGCCACGACGCGCGCTTCTTTC  
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Db 13071 CTGCAAGACGAGGCGCGCTATCGTGGCTGGCCACGACGCGCGCTTCTTTC  
|||  
Qy 2916 GTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGGGAAGTG  
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Db 13131 GTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGGGAAGTG  
|||  
Qy 2976 CAGGATCTCTGTCTCATCTCACTTGTCTCCGCGAGAAAGTATCCATCATGGCT  
|||  
Db 13191 CAGGATCTCTGTCTCATCTCACTTGTCTCCGCGAGAAAGTATCCATCATGGCT  
|||  
Qy 3036 ATGCGCGGCTGCATACGCTTGTATCCGCTACTCTGCGCAATTCGACCAAGAGCG  
|||  
Db 13251 ATGCGCGGCTGCATACGCTTGTATCCGCTACTCTGCGCAATTCGACCAAGAGCG  
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Qy 3096 CGCATCGAGCGAGCAGCTACTCGGATGGAGCGGCTCTTGTGATCAGGATGAT  
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Db 13311 CGCATCGAGCGAGCAGCTACTCGGATGGAGCGGCTCTTGTGATCAGGATGAT  
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Qy 3156 GAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCGAGGCTCAAGCGGAGC  
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Qy 3216 GACGCGAGGATCTCGTGTGTGACCCATGGCGATGCTGCTTTCGCGAAATCATG  
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Db 13431 GACGCGAGGATCTCGTGTGTGACCCATGGCGATGCTGCTTTCGCGAAATCATG  
|||  
Qy 3276 AATGCGCGCTTTCTGGAATTCATCGACTGTGGCGGCTGGGTGGGGGAGCGCG  
|||  
Db 13491 AATGCGCGCTTTCTGGAATTCATCGACTGTGGCGGCTGGGTGGGGGAGCGCG  
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Qy 3336 GACATAGCTTGGCTTACCGGTGATTTGCTGAAGAGCTTGGCGGCAATGGGCT  
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Db 13551 GACATAGCTTGGCTTACCGGTGATTTGCTGAAGAGCTTGGCGGCAATGGGCT  
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Qy 3396 TTCTCTGTGCTTTACGGTATCCGCTCCCGATTCGCAAGCGCATTCGCTTCTAT  
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Db 13611 TTCTCTGTGCTTTACGGTATCCGCTCCCGATTCGCAAGCGCATTCGCTTCTAT  
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Qy 3456 CTGCAAGGTTCTTCTGAGCGGGAATCTGGGGTTCGAAATGACCGACCAAGGGA  
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Db 13671 CTGCAAGGTTCTTCTGAGCGGGAATCTGGGGTTCGAAATGACCGACCAAGGGA  
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Qy 3516 ACTGCGCATACGAGATTTGATTTCCACCGCGGCTTCTATGAAAGGTTGGGCT  
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Qy 3576 TCGTTTTCCGGGAACGCGGCTGGAGATGATCTCTCCAGCGCGGGGATCTCATGTGG  
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Db 13741 -----  
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Qy 3636 TCGCCCACTTAGGGGAGGCTTAATGAAACACGGAAGGAGACAAATACCGGAAG  
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Db 13741 -----  
|||  
Qy 3696 CGCATGACGCAATAAAGAGCAGAAATAAAGCAAGCTGTTGGGTGCTTTGT  
|||  
Db 13741 -----  
|||  
Qy 3756 ACGCGGGGTTCCGTTCCAGGGCTGGCACTCTGTGTGATACCCCAACGAGACCGCA



1590	Dc	GTCCGCTTCTCCCTTCGGGAAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGTATCT	14649
1836	Qy	CAGTTCCGGTGTAGTGGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGGTTCAGCC	4895
1651	Dc	CAGTTCCGGTGTAGTGGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGGTTCAGCC	14709
1851	Qy	CACCGCTGGCCTTAATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAAGACACGACTT	4955
1711	Dc	CACCGCTGGCCTTAATCCGGTAACTATCGTCTTGAGTCCAAACCCGGTAAAGACACGACTT	14769
1931	Qy	ATCGCCACTCGCAGCAGCCACTGGTAAACAGGATTACGACAGCGAGGTATGTAGGCGGTGC	5015
1771	Dc	ATCGCCACTCGCAGCAGCCACTGGTAAACAGGATTACGACAGCGAGGTATGTAGGCGGTGC	14829
1011	Qy	TACAGAGTTCTTCAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT	5075
1830	Dc	TACAGAGTTCTTCAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT	14889
1071	Qy	CTGGCTCTGCTGAAGCAGTTACCTTCGGAAAAAGAGTTGTAGCTCTTGATCCGGCAA	5135
1890	Dc	CTGGCTCTGCTGAAGCAGTTACCTTCGGAAAAAGAGTTGTAGCTCTTGATCCGGCAA	14949
1131	Qy	AUAAACACACCGCTGTAGCGGTGTTTTTTGTTTGCACAGCAGCAGATTACGCGCAGAAA	5195
1950	Dc	AUAAACACACCGCTGTAGCGGTGTTTTTTGTTTGCACAGCAGCAGATTACGCGCAGAAA	15009
1191	Qy	AAAGGATCTCAAGAAAGATCTTTTGATCTTTTCTACGGGCTCTGACGCTCAGTCGAAAGA	5255
1010	Dc	AAAGGATCTCAAGAAAGATCTTTTGATCTTTTCTACGGGCTCTGACGCTCAGTCGAAAGA	15069
1251	Qy	AAACTCAGTTAAGGATTTTGTGTATGAGATTTATCAAAAAAGATCTTCACTAGATCCT	5315
1070	Dc	AAACTCAGTTAAGGATTTTGTGTATGAGATTTATCAAAAAAGATCTTCACTAGATCCT	15129
1311	Qy	TTTAAATTAATAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGTCTGA	5375
1230	Dc	TTTAAATTAATAAATGAAGTTTAAATCAATCTAAAGTATATATGAGTAAACTTGTCTGA	15189
1371	Qy	CAGTTACCAATGCTTAATCAGTCAGGCACTATCTCAGCGATCTGTCTATTTCGTTCAATC	5435
1190	Dc	CAGTTACCAATGCTTAATCAGTCAGGCACTATCTCAGCGATCTGTCTATTTCGTTCAATC	15249
1431	Qy	CATAGTTGCCGTGATCTCCCGTGTGTAGATAACTACGATACGGAGGGCTTACCATCTGG	5495
1250	Dc	CATAGTTGCCGTGATCTCCCGTGTGTAGATAACTACGATACGGAGGGCTTACCATCTGG	15309
1491	Qy	CTCCAGTGTGCAATGATACCGCGAGACCCAGCTCACCGGCTCCAGATTATCAGCAAT	5555
1310	Dc	CTCCAGTGTGCAATGATACCGCGAGACCCAGCTCACCGGCTCCAGATTATCAGCAAT	15369
1551	Qy	AAACACGACGCGGAGGGCCGAGCGCAGAGTGGTCTCTGCAACTTTATCCGCTCCAT	5615
1370	Dc	AAACACGACGCGGAGGGCCGAGCGCAGAGTGGTCTCTGCAACTTTATCCGCTCCAT	15429
1611	Qy	CGAGTCTATTAAATTTGTTGCCGGAAGCTAGATAGTATTGCTCGCAAGTTAATGAGTTGCG	5675
1430	Dc	CGAGTCTATTAAATTTGTTGCCGGAAGCTAGATAGTATTGCTCGCAAGTTAATGAGTTGCG	15489
1671	Qy	CAAGTTGTTGCCATTGCTACAGGCATCTGTGTGTACGCTCGTGGTTGGTATGGCTTC	5735
1490	Dc	CAAGTTGTTGCCATTGCTACAGGCATCTGTGTGTACGCTCGTGGTTGGTATGGCTTC	15549
1731	Qy	AUUCAGCTCCGGTTTCCCAACGATCAAGGGGAGTTACATGATCCCCATGTTGTGCAAAA	5795
1550	Dc	AUUCAGCTCCGGTTTCCCAACGATCAAGGGGAGTTACATGATCCCCATGTTGTGCAAAA	15609
1791	Qy	ATCGGTTAGTCTCTTCCGTCCTCCGATCGTTGTGAGAAGTAAAGTTGGCGCAGTGTATC	5855
1610	Dc	ATCGGTTAGTCTCTTCCGTCCTCCGATCGTTGTGAGAAGTAAAGTTGGCGCAGTGTATC	15669
1851	Qy	AUUCATGGTTATGGCAGCACTGATATTAATTTCTCTTACTGTATGCCATCCGTAAGATGTT	5915
1670	Dc	AUUCATGGTTATGGCAGCACTGATATTAATTTCTCTTACTGTATGCCATCCGTAAGATGTT	15729

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GGATCTCTGTGTCATCTCACTTGTCTCTCGCGAGAAAGTATCCATCATGGCTGATGCA 3035  
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CATCGAGCGGACGCTACGATCGGATGGAAGCGGCTCTGTGATCAGGATGATCTGGAC 3155  
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CATAGCGTTGGCTACCCGTTGATATTGCTGAAGAGCTTGGCGCGAATGGGCTGACCGC 3395  
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----- 13740  
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----- 13740  
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Db 13741 -----  
Qy 3756 ACGCGGGGTTCCGTCCACAGGGCTGGCACTCTGTGATACCCCAACGAGACCCCA  
Db 13741 -----  
Qy 3816 CCAATACGCCCGCGGTTCTTCTCTTCCCCACCCCAACCCCAAGTTCCGGGTGA  
Db 13741 -----  
Qy 3876 AGGCTCGCAGCAACCGTCCGGCGCGAGGCCCTGCCATAGCCTCAGTGTACG  
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[illegible]

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RESULT 10  
US-08-404-796-1  
; Sequence 1, Application US/08404796  
; Patent No. 6015686  
; GENERAL INFORMATION:  
; APPLICANT: Dubensky Jr, Thomas W  
; APPLICANT: Polo, John M.  
; APPLICANT: Ibanez, Carlos E.  
; APPLICANT: Chang, Stephen M.W.  
; APPLICANT: Jolly, Douglas J.  
; APPLICANT: Driver, David A.  
; APPLICANT: Belli, Barbara A.  
; TITLE OF INVENTION: EUKARYOTIC LAYERED VECTOR INITIATION SYSTE  
; NUMBER OF SEQUENCES: 128  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: SEED and BERRY LLP  
; STREET: 6300 Columbia Center, 701 Fifth Avenue  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: US  
; ZIP: 98104-7092  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/404,796  
; APPLICATION NUMBER: 15-MAR-1995  
; FILING DATE: 15-MAR-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McMAsters, David D.  
; REGISTRATION NUMBER: 33,963  
; REFERENCE/DOCKET NUMBER: 930049.423C5 / 1146.006  
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